

GenCore version 5.1.4.p5-4578
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Om protein - protein search, using sw model
Run on: April 22, 2003, 17:11:26 ; Search time 36 Seconds
(without alignments)

Perfect score: US-09-910-033a-2
Sequence: 1 MSNRDCKVAILTGGTLCIG..... NESKFATGSEFVVDDGYTAQ 252
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250520 residues
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Total number of hits satisfying chosen parameters: 908470
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Database : A_Geneset_101002:*

- 1: /SIDS2/gcdata/genesed/geneseq/geneseq-emb1/AA1980.DAT:*
- 2: /SIDS2/gcdata/genesed/geneseq/geneseq-emb1/AA1981.DAT:*
- 3: /SIDS2/gcdata/genesed/geneseq/geneseq-emb1/AA1983.DAT:*
- 4: /SIDS2/gcdata/genesed/geneseq/geneseq-emb1/AA1984.DAT:*
- 5: /SIDS2/gcdata/genesed/geneseq/geneseq-emb1/AA1985.DAT:*
- 6: /SIDS2/gcdata/genesed/geneseq/geneseq-emb1/AA1987.DAT:*
- 7: /SIDS2/gcdata/genesed/geneseq/geneseq-emb1/AA1987.DAT:*
- 8: /SIDS2/gcdata/genesed/geneseq/geneseq-emb1/AA1988.DAT:*
- 9: /SIDS2/gcdata/genesed/geneseq/geneseq-emb1/AA1989.DAT:*
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- 11: /SIDS2/gcdata/genesed/geneseq/geneseq-emb1/AA1991.DAT:*
- 12: /SIDS2/gcdata/genesed/geneseq/geneseq-emb1/AA1992.DAT:*
- 13: /SIDS2/gcdata/genesed/geneseq/geneseq-emb1/AA1993.DAT:*
- 14: /SIDS2/gcdata/genesed/geneseq/geneseq-emb1/AA1994.DAT:*
- 15: /SIDS2/gcdata/genesed/geneseq/geneseq-emb1/AA1995.DAT:*
- 16: /SIDS2/gcdata/genesed/geneseq/geneseq-emb1/AA1996.DAT:*
- 17: /SIDS2/gcdata/genesed/geneseq/geneseq-emb1/AA1997.DAT:*
- 18: /SIDS2/gcdata/genesed/geneseq/geneseq-emb1/AA1998.DAT:*
- 19: /SIDS2/gcdata/genesed/geneseq/geneseq-emb1/AA1999.DAT:*
- 20: /SIDS2/gcdata/genesed/geneseq/geneseq-emb1/AA2000.DAT:*
- 21: /SIDS2/gcdata/genesed/geneseq/geneseq-emb1/AA2001.DAT:*
- 22: /SIDS2/gcdata/genesed/geneseq/geneseq-emb1/AA2002.DAT:*
- 23: /SIDS2/gcdata/genesed/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8 Query Match Length DB ID Description
Result No. Score Match Length DB ID Description
Recombinant enzyme
Lactobacillus brev
Lactobacillus kefir
Protein with acetyl
(R)-2-octanol dehy
Bacillus D-arabin
Bacillus epi
Staphylococcus aur
Staphylococcus lactic
Lactococcus lactic
Glucose dehydrogen

11	366.5	28.4	23	AAE20115	Lactobacillus rham
12	364.5	28.3	261	11 AAR04044	Glucose dehydrogen
13	364.5	28.3	261	13 AAR24018	Thermostable gluco
14	364	28.2	251	22 AAU3193	Staphylococcus aur
15	363.5	28.2	272	21 AAB10740	B. megaterium gluc
16	363.5	28.2	340	21 AAB10741	H. ghilianii/B. me
17	360.5	27.9	261	11 AAR03846	Modified glucose d
18	359.5	27.9	261	13 AAR27756	NAD affinity gluco
19	358.5	27.8	261	9 AAP0590	Pseudomonas aerugi
20	358.5	27.8	261	21 AAY96271	Staphylococcus epi
21	358.5	27.8	261	9 AAY34424	B. subtilis glucos
22	356.5	27.6	261	9 AAP0063	Amino acid sequenc
23	352.5	27.3	22	22 AAB3032	Glucose dehydrogen
24	351	27.2	286	22 AAU36267	S. epidermidis ope
25	348.5	27.0	263	23 ABP39667	Pseudomonas aerugi
26	345	26.7	305	22 AAB81644	Staphylococcus epi
27	344	26.7	270	21 AAB22558	S. epidermidis op
28	344	26.7	303	23 ABP92264	Human ORKX ORK2322
29	341	26.4	274	23 ABP39586	Herbicidally activ
30	340	26.4	270	20 AAU41761	Staphylococcus epi
31	340	26.4	270	21 AAU44311	Human PRO474 prote
32	340	26.4	270	21 ABP34056	Human PRO474 prote
33	340	26.4	270	22 AAU38108	Novel human secret
34	340	26.4	279	22 AAU18296	Novel human secret
35	336.5	26.1	271	22 AAU137794	Human endocrine po
36	336.5	26.1	272	22 AAU38086	Streptococcus pneu
37	334.5	25.9	288	22 AAU28296	Streptococcus pneu
38	334.5	25.9	280	22 AAU29449	Novel human secret
39	330.5	25.6	254	23 ABP30228	Novel human secret
40	330.5	25.6	263	23 ABP28167	Streptococcus poly
41	330.5	25.6	270	23 ABP26580	Streptococcus poly
42	330.5	25.6	277	21 AAU54415	Secoisolariciresin
43	324	25.1	253	23 ABB0010	Listeria monocytog
44	324	27.4	23 AAU22161	Ramoplanin biosynth	
45	324	25.1	336	16 AAU06488	Maize Ts2 sequence

ALIGNMENTS

RESULT 1
ID AA016940 standard; Protein: 252 AA.

XX AAC AA016940;
XX DT 16-MAY-2002 (first entry)
XX DE Recombinant enzyme with increased NAD(H) acceptance.

XX KW NAD(H) acceptance enzyme; reduced nicotinamide-adenine dinucleotide;
KW ketone; alcohol; enantiomerically enriched.
XX OS Synthetic.
XX
FT Key Location/Qualifiers
FT Misc-difference 38 /note= "wild-type Gly substituted by Asp".

XX PN EP1176203-A1.
XX PD 30-JAN-2002.
XX PF 20-JUN-2001; 2001EP-0114953.
XX PR 27-JUL-2000; 2000EP-1037101.
XX PA (DEGS) DEGUSSA AG.
XX PI Riebel, B., Hummel, W., Bommarius, A.;
XX DR WPT; 2002-173122/23.

DR N-PSDB; AAL45006.
 PT New recombinant enzyme, useful for enantioselective synthesis of e.g. alcohols, has increased nicotinamide-adenine dinucleotide acceptance as result of specific mutation -
 XX
 PS Disclosure; Page 7-8; 23pp; German.
 CC The present invention relates to a recombinant enzyme with higher NAD(H) (reduced) nicotinamide-adenine dinucleotide acceptance than the wild type, and which has at least one neutral amino acid exchanged for an acidic amino acid, while retaining the basic amino acid in the co-enzyme binding site. The enzyme can be used to prepare enantioselectively enriched organic compounds, especially enantioselective reduction of ketones or oxidation of alcohols. The present sequence is the enzyme of the invention.
 CC
 XX Sequence 252 AA:
 Query Match 100.0%; Score 1290; DB 23; Length 252;
 Best Local Similarity 100.0%; Pred. No. 4.3e-11; Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MUSRUDKGKVAITGGTGGIGLATAKTFVEGAKVMTDRHSOGEKAASKVSPDQI OFF 60
 1 MSNRLDGKVAITGGTGGIGLATAKTFVEGAKVMTDRHSOGEKAASKVSPDQI OFF 60
 QY 61 QHDSSDEGWTKLFDATKEAFGVSTLYNNAGAVNKSVEETTAENRKLLAVNLDCVFF 120
 61 QHDSSDEGWTKLFDATKEAFGVSTLYNNAGAVNKSVEETTAENRKLLAVNLDCVFF 120
 QY 121 GTRLGIGRMKNKGIGASINMSIEGVGDPSEGVLGAYNASKAVRIMSKSAALDCALKDY 180
 121 GTRLGIGRMKNKGIGASINMSIEGVGDPSEGVLGAYNASKAVRIMSKSAALDCALKDY 180
 QY 181 VRVNTVIRGYIKTPVLDLPGAEAMSQRTKTPMGHIGEPAIDAYCIVYLASNESKATG 240
 181 VRVNTVIRGYIKTPVLDLPGAEAMSQRTKTPMGHIGEPAIDAYCIVYLASNESKATG 240
 Db 241 SEFVWDGGYTAQ 252
 241 SEFVWDGGYTAQ 252

SQ

Query Match 100.0%; Score 1290; DB 23; Length 252;

Best Local Similarity 100.0%; Pred. No. 4.3e-11; Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 MUSRUDKGKVAITGGTGGIGLATAKTFVEGAKVMTDRHSOGEKAASKVSPDQI OFF 60

Db

1 MSNRLDGKVAITGGTGGIGLATAKTFVEGAKVMTDRHSOGEKAASKVSPDQI OFF 60

QY

61 QHDSSDEGWTKLFDATKEAFGVSTLYNNAGAVNKSVEETTAENRKLLAVNLDCVFF 120

Db

61 QHDSSDEGWTKLFDATKEAFGVSTLYNNAGAVNKSVEETTAENRKLLAVNLDCVFF 120

QY

121 GTRLGIGRMKNKGIGASINMSIEGVGDPSEGVLGAYNASKAVRIMSKSAALDCALKDY 180

Db

121 GTRLGIGRMKNKGIGASINMSIEGVGDPSEGVLGAYNASKAVRIMSKSAALDCALKDY 180

QY

181 VRVNTVIRGYIKTPVLDLPGAEAMSQRTKTPMGHIGEPAIDAYCIVYLASNESKATG 240

Db

181 VRVNTVIRGYIKTPVLDLPGAEAMSQRTKTPMGHIGEPAIDAYCIVYLASNESKATG 240

QY

241 SEFVWDGGYTAQ 252

Db

241 SEFVWDGGYTAQ 252

SQ

Sequence 252 AA:

Query Match 99.0%; Score 1277; DB 18; Length 252;

Best Local Similarity 99.2%; Pred. No. 7.9e-11; Matches 250; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY

1 MUSRUDKGKVAITGGTGGIGLATAKTFVEGAKVMTDRHSOGEKAASKVSPDQI OFF 60

Db

1 MUSRUDKGKVAITGGTGGIGLATAKTFVEGAKVMTDRHSOGEKAASKVSPDQI OFF 60

QY

61 QHDSSDEGWTKLFDATKEAFGVSTLYNNAGAVNKSVEETTAENRKLLAVNLDCVFF 120

Db

61 QHDSSDEGWTKLFDATKEAFGVSTLYNNAGAVNKSVEETTAENRKLLAVNLDCVFF 120

QY

121 GTRLGIGRMKNKGIGASINMSIEGVGDPSEGVLGAYNASKAVRIMSKSAALDCALKDY 180

Db

121 GTRLGIGRMKNKGIGASINMSIEGVGDPSEGVLGAYNASKAVRIMSKSAALDCALKDY 180

QY

181 VRVNTVIRGYIKTPVLDLPGAEAMSQRTKTPMGHIGEPAIDAYCIVYLASNESKATG 240

Db

181 VRVNTVIRGYIKTPVLDLPGAEAMSQRTKTPMGHIGEPAIDAYCIVYLASNESKATG 240

QY

241 SEFVWDGGYTAQ 252

Db

241 SEFVWDGGYTAQ 252

SQ

Sequence 252 AA:

Query Match 99.0%; Score 1277; DB 18; Length 252;

Best Local Similarity 99.2%; Pred. No. 7.9e-11; Matches 250; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY

1 MUSRUDKGKVAITGGTGGIGLATAKTFVEGAKVMTDRHSOGEKAASKVSPDQI OFF 60

Db

1 MUSRUDKGKVAITGGTGGIGLATAKTFVEGAKVMTDRHSOGEKAASKVSPDQI OFF 60

QY

61 QHDSSDEGWTKLFDATKEAFGVSTLYNNAGAVNKSVEETTAENRKLLAVNLDCVFF 120

Db

61 QHDSSDEGWTKLFDATKEAFGVSTLYNNAGAVNKSVEETTAENRKLLAVNLDCVFF 120

QY

121 GTRLGIGRMKNKGIGASINMSIEGVGDPSEGVLGAYNASKAVRIMSKSAALDCALKDY 180

Db

121 GTRLGIGRMKNKGIGASINMSIEGVGDPSEGVLGAYNASKAVRIMSKSAALDCALKDY 180

QY

181 VRVNTVIRGYIKTPVLDLPGAEAMSQRTKTPMGHIGEPAIDAYCIVYLASNESKATG 240

Db

181 VRVNTVIRGYIKTPVLDLPGAEAMSQRTKTPMGHIGEPAIDAYCIVYLASNESKATG 240

QY

241 SEFVWDGGYTAQ 252

Db

241 SEFVWDGGYTAQ 252

SQ

Sequence 252 AA:

Query Match 99.0%; Score 1277; DB 18; Length 252;

Best Local Similarity 99.2%; Pred. No. 7.9e-11; Matches 250; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY

1 MUSRUDKGKVAITGGTGGIGLATAKTFVEGAKVMTDRHSOGEKAASKVSPDQI OFF 60

Db

1 MUSRUDKGKVAITGGTGGIGLATAKTFVEGAKVMTDRHSOGEKAASKVSPDQI OFF 60

QY

61 QHDSSDEGWTKLFDATKEAFGVSTLYNNAGAVNKSVEETTAENRKLLAVNLDCVFF 120

Db

61 QHDSSDEGWTKLFDATKEAFGVSTLYNNAGAVNKSVEETTAENRKLLAVNLDCVFF 120

QY

121 GTRLGIGRMKNKGIGASINMSIEGVGDPSEGVLGAYNASKAVRIMSKSAALDCALKDY 180

Db

121 GTRLGIGRMKNKGIGASINMSIEGVGDPSEGVLGAYNASKAVRIMSKSAALDCALKDY 180

QY

181 VRVNTVIRGYIKTPVLDLPGAEAMSQRTKTPMGHIGEPAIDAYCIVYLASNESKATG 240

Db

181 VRVNTVIRGYIKTPVLDLPGAEAMSQRTKTPMGHIGEPAIDAYCIVYLASNESKATG 240

QY

241 SEFVWDGGYTAQ 252

Db

241 SEFVWDGGYTAQ 252

SQ

Sequence 252 AA:

Query Match 99.0%; Score 1277; DB 18; Length 252;

Best Local Similarity 99.2%; Pred. No. 7.9e-11; Matches 250; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY

1 MUSRUDKGKVAITGGTGGIGLATAKTFVEGAKVMTDRHSOGEKAASKVSPDQI OFF 60

Db

1 MUSRUDKGKVAITGGTGGIGLATAKTFVEGAKVMTDRHSOGEKAASKVSPDQI OFF 60

QY

61 QHDSSDEGWTKLFDATKEAFGVSTLYNNAGAVNKSVEETTAENRKLLAVNLDCVFF 120

Db

61 QHDSSDEGWTKLFDATKEAFGVSTLYNNAGAVNKSVEETTAENRKLLAVNLDCVFF 120

QY

121 GTRLGIGRMKNKGIGASINMSIEGVGDPSEGVLGAYNASKAVRIMSKSAALDCALKDY 180

Db

121 GTRLGIGRMKNKGIGASINMSIEGVGDPSEGVLGAYNASKAVRIMSKSAALDCALKDY 180

QY

181 VRVNTVIRGYIKTPVLDLPGAEAMSQRTKTPMGHIGEPAIDAYCIVYLASNESKATG 240

Db

181 VRVNTVIRGYIKTPVLDLPGAEAMSQRTKTPMGHIGEPAIDAYCIVYLASNESKATG 240

QY

241 SEFVWDGGYTAQ 252

Db

241 SEFVWDGGYTAQ 252

SQ

Sequence 252 AA:

Query Match 99.0%; Score 1277; DB 18; Length 252;

Best Local Similarity 99.2%; Pred. No. 7.9e-11; Matches 250; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY

1 MUSRUDKGKVAITGGTGGIGLATAKTFVEGAKVMTDRHSOGEKAASKVSPDQI OFF 60

Db

1 MUSRUDKGKVAITGGTGGIGLATAKTFVEGAKVMTDRHSOGEKAASKVSPDQI OFF 60

QY

61 QHDSSDEGWTKLFDATKEAFGVSTLYNNAGAVNKSVEETTAENRKLLAVNLDCVFF 120

Db

61 QHDSSDEGWTKLFDATKEAFGVSTLYNNAGAVNKSVEETTAENRKLLAVNLDCVFF 120

QY

121 GTRLGIGRMKNKGIGASINMSIEGVGDPSEGVLGAYNASKAVRIMSKSAALDCALKDY 180

Db

121 GTRLGIGRMKNKGIGASINMSIEGVGDPSEGVLGAYNASKAVRIMSKSAALDCALKDY 180

QY

181 VRVNTVIRGYIKTPVLDLPGAEAMSQRTKTPMGHIGEPAIDAYCIVYLASNESKATG 240

Db

181 VRVNTVIRGYIKTPVLDLPGAEAMSQRTKTPMGHIGEPAIDAYCIVYLASNESKATG 240

QY

241 SEFVWDGGYTAQ 252

Db

241 SEFVWDGGYTAQ 252

SQ

Sequence 252 AA:

Query Match 99.0%; Score 1277; DB 18; Length 252;

Best Local Similarity 99.2%; Pred. No. 7.9e-11; Matches 250; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY

1 MUSRUDKGKVAITGGTGGIGLATAKTFVEGAKVMTDRHSOGEKAASKVSPDQI OFF 60

Db

1 MUSRUDKGKVAITGGTGGIGLATAKTFVEGAKVMTDRHSOGEKAASKVSPDQI OFF 60

QY

61 QHDSSDEGWTKLFDATKEAFGVSTLYNNAGAVNKSVEETTAENRKLLAVNLDCVFF 120

Db

61 QHDSSDEGWTKLFDATKEAFGVSTLYNNAGAVNKSVEETTAENRKLLAVNLDCVFF 120

QY

121 GTRLGIGRMKNKGIGASINMSIEGVGDPSEGVLGAYNASKAVRIMSKSAALDCALKDY 180

Db

121 GTRLGIGRMKNKGIGASINMSIEGVGDPSEGVLGAYNASKAVRIMSKSAALDCALKDY 180

QY

181 VRVNTVIRGYIKTPVLDLPGAEAMSQRTKTPMGHIGEPAIDAYCIVYLASNESKATG 240

Db

181 VRVNTVIRGYIKTPVLDLPGAEAMSQRTKTPMGHIGEPAIDAYCIVYLASNESKATG 240

QY

241 SEFVWDGGYTAQ 252

Db

241 SEFVWDGGYTAQ 252

SQ

Sequence 252 AA:

Query Match 99.0%; Score 1277; DB 18; Length 252;

Best Local Similarity 99.2%; Pred. No. 7.9e-11; Matches 250; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY

1 MUSRUDKGKVAITGGTGGIGLATAKTFVEGAKVMTDRHSOGEKAASKVSPDQI OFF 60

Db

1 MUSRUDKGKVAITGGTGGIGLATAKTFVEGAKVMTDRHSOGEKAASKVSPDQI OFF 60

QY

61 QHDSSDEGWTKLFDATKEAFGVSTLYNNAGAVNKSVEETTAENRKLLAVNLDCVFF 120

Db

61 QHDSSDEGWTKLFDATKEAFGVSTLYNNAGAVNKSVEETTAENRKLLAVNLDCVFF 120

QY

121 GTRLGIGRMKNKGIGASINMSIEGVGDPSEGVLGAYNASKAVRIMSKSAALDCALKDY 180

Db

121 GTRLGIGRMKNKGIGASINMSIEGVGDPSEGVLGAYNASKAVRIMSKSAALDCALKDY 180

QY

181 VRVNTVIRGYIKTPVLDLPGAEAMSQRTKTPMGHIGEPAIDAYCIVYLASNESKATG 240

Db

181 VRVNTVIRGYIKTPVLDLPGAEAMSQRTKTPMGHIGEPAIDAYCIVYLASNESKATG 240

QY

241 SEFVWDGGYTAQ 252

Db

241 SEFVWDGGYTAQ 252

SQ

Sequence 252 AA:

Query Match 99.0%; Score 1277; DB 18; Length 252;

Best Local Similarity 99.2%; Pred. No. 7.9e-11; Matches 250; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY

1 MUSRUDKGKVAITGGTGGIGLATAKTFVEGAKVMTDRHSOGEKAASKVSPDQI OFF 60

Db

1 MUSRUDKGKVAITGGTGGIGLATAKTFVEGAKVMTDRHSOGEKAASKVSPDQI OFF 60

QY

61 QHDSSDEGWTKLFDATKEAFGVSTLYNNAGAVNKSVEETTAENRKLLAVNLDCVFF 120

Db

61 QHDSSDEGWTKLFDATKEAFGVSTLYNNAGAVNKSVEETTAENRKLLAVNLDCVFF 120

QY

121 GTRLGIGRMKNKGIGASINMSIEGVGDPSEGVLGAYNASKAVRIMSKSAALDCALKDY 180

Db

121 GTRLGIGRMKNKGIGASINMSIEGVGDPSEGVLGAYNASKAVRIMSKSAALDCALKDY 180

QY

181 VRVNTVIRGYIKTPVLDLPGAEAMSQRTKTPMGHIGEPAIDAYCIVYLASNESKATG 240

Db

181 VRVNTVIRGYIKTPVLDLPGAEAMSQRTKTPMGHIGEPAIDAYCIVYLASNESKATG 240

QY

241 SEFVWDGGYTAQ 252

Db

241 SEFVWDGGYTAQ 252

SQ

Sequence 252 AA:

Query Match 99.0%; Score 1277; DB 18; Length 252;

Best Local Similarity 99.2%; Pred. No. 7.9e-11; Matches 250; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY

1 MUSRUDKGKVAITGGTGGIGLATAKTFVEGAKVMTDRHSOGEKAASKV

FT Misc-difference 51
 FT /note- "not defined in specification"
 FT Misc-difference 52
 FT /note- "not defined in specification"
 FT Misc-difference 53
 FT /note- "not defined in specification"
 FT Misc-difference 54
 FT /note- "not defined in specification"
 FT Misc-difference 55
 FT /note- "not defined in specification"
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 FT /note- "not defined in specification"
 FT Misc-difference 57
 FT /note- "not defined in specification"
 FT Misc-difference 58
 FT /note- "not defined in specification"
 FT Misc-difference 59
 FT /note- "not defined in specification"
 FT Misc-difference 60
 FT /note- "not defined in specification"
 FT Misc-difference 61
 FT /note- "not defined in specification"
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 FT /note- "not defined in specification"
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 FT /note- "not defined in specification"
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 FT /note- "not defined in specification"
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 FT /note- "not defined in specification"
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 FT /note- "not defined in specification"
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 FT /note- "not defined in specification"
 FT Misc-difference 71
 FT /note- "not defined in specification"
 FT Misc-difference 130
 FT /note- "not defined in specification"
 FT Misc-difference 131
 FT /note- "not defined in specification"
 PN EP796914-A2.
 XX
 PD 24-SEP-1997.
 XX
 PF 20-MAR-1997; 97EP-0104814.
 XX
 PR 21-MAR-1996; 96DE-4010984.
 XX
 PA (BOEP) BOEHRINGER MANNHEIM GMBH.
 XX
 PT Hummel W, Riebel B;
 DR WPI; 1997-459831/43.
 XX
 PT Lactobacillus brevis alcohol dehydrogenase - useful for production
 PT of optically active alcohol(s)
 XX
 Example 8; Pages 28-30; 34pp; German.
 PS
 XX
 CC The present Lactobacillus kefir alcohol dehydrogenase (ADH) was used in the isolation of a L. brevis ADH, which retains at least 95% of its activity after 30 minutes at 20-60 degrees C and can be purified to a specific activity of at least 400 U/mg. The enzyme can be used to produce (R)-alcohols by enantioselective reduction of ketones of formula R1-CO-R2, where R1 and R2 = hydrogen (sic) or 1-20C alkyl, alkenyl, aryl or arylidyl (sic) optionally
 CC substituted by halogen, NO2, OH or 1-20C alkoxy, "an optionally saturated 1-10C alkylene group, which is substituted by saturated, unsaturated or aromatic nitrogen, oxygen or sulphur heterocycles, or may be an optionally substituted polycondensed saturated and/or aromatic group" (sic) in the presence of the enzyme or cells by incubating it at 20-60 degrees C for 0.25-3 hours, or (S)-alcohols by incubating a racemic alcohol of formula R1-CHOH-R2 in the presence of the enzyme or cells containing it at 20-60 degrees C for 0.25-3 hours.
 CC R1-CHOH-R2 in the presence of the enzyme or cells containing it at 20-60 degrees C for 0.25-3 hours.
 XX
 SO Sequence 251 AA;

Query Match 79.0%; Score 1019; DB 18; Length 251;
 Best local Similarity 80.5%; Pred. No. 9.3e-91;
 Matches 202; Conservative 14; Mismatches 35; Indels 0; Gaps 0;
 QY 2 SRLDGKVAITRGGTIGLATAKFEVAGAKMIDHSDVGEKAASVGTGTPQIOFFQ 61
 Db 1 TDRLGKVAITRGGTIGLGLAIDKFVAGAKVITGHRADGEKXXXKXXXXXX 60

QY 62 HDSSDEGWTKLFDATKEAAGPVSTLYNAGIAYVNKSSETTAEWRKILAVNLGVPG 121
 Db 61 XXXXXXXXXXXXLFDATEAAGPVTTWVNAGIAYVNKSSETTAEWRKLSVNLDGVPG 120

QY 122 TRIGIORMKNGLIGASINNMSSTEGVNDPSLIGAYNASKGAVIMSKAALDCALKDY 181
 Db 121 TRIGIOMKNGLIGASINNMSSTEGVNDPSLIGAYNASKGAVIMSKAALDCALKDY 180

QY 182 RNTVHGEYIKTPLWDPPGAERMSQTTPKGHIGSPNDIAYICVLASNSKFGS 241
 Db 181 RNTVHGEYIKTPLWDPPGAERMSQTTPKGHIGSPNDIAYICVLASNSKFGS 240

QY 242 EFVVDGGYTAQ 252
 Db 241 EFVVDGGYTAQ 251

RESULT 4
 AAB49773
 ID AAB49773 standard; protein; 254 AA.
 XX
 AC: AAB49773;
 XX
 DT 23-APR-2001 (first entry)
 XX
 DE Protein with acetylpyridine derivative reducing action.
 XX
 KW Optically-active pyridineethanol derivative; asymmetric reduction.
 XX
 OS Candida maris.
 XX
 PN WO200105996 A1.
 XX
 PD 25-JAN-2001.
 XX
 PF 28-JUN-2000; 2000WO-JP04237.
 XX
 PR 21-JUL-1999; 99JP-0206503.
 XX
 PA (KANF) KANERA CORP.
 XX
 PI Kawano S, Horikawa M, Yasohara Y, Hasegawa J;
 XX
 DR WPI; 2001-159546/16.
 DR N-PSDB; AAF29375.
 XX
 PT Efficient, high-yielding preparation of optically-active pyridineethanol derivatives by stereoselectively reducing acetylpyridine derivatives e.g. with enzyme having asymmetric reduction activity, for pharmaceutical intermediates.
 XX
 PS Claim 14; Fig 1; 76pp; Japanese.

This invention relates to a process for producing optically-active pyridineethanol derivatives by stereoselectively reducing acetylpyridin derivatives with an enzyme or enzyme source having asymmetric reduction activity. The process is efficient and high yielding to give R and S isomers by suitable manipulation. The method is for the preparation of optically-active pyridineethanol derivatives by stereoselectively reducing acetylpyridine derivatives, and also similarly for their polycyclic analogues, for use as pharmaceutical and agrochemical intermediates, as well as in fine chemical production. The present sequence represents the amino acid sequence of the enzyme used in the process which has acetylpyridine derivative reducing action.

Matches	Best Local Similarity	Score	DB	Length	Gaps
104	Conservative	40.2%	Score: 456; DB: 22;	Length: 254;	
1	MSNRLDGKVAITTGTGIGLIAKTFVEEGKRVMTD	35.3%			
1	MSYNFANKVLUITGGLSSGIGLAVAKKFQLQGAKVTISD	36.5%			
55	DOIQFQHDSSDEDGWKLKFDTATEKFGPVSTLVNNAGIAVNKSVEETTAENRKLAVN	35.3%			
61	N-VOYIQLADSKRREADNEKLTSBTLSAFGDLDVYCANAGIATQTOTISYDVRKUSIN	35.3%			
115	LDGVFFGCTRLGIQRMKNKGGLGASINNMSIEFVGDBSLIGAYNAASKGAVRIMSKAALDC	35.3%			
120	LDGVFEMLDKLAAQYELSKNPKGAIVNNGSIHSYVAAPGLSHGAAKGKLQTOMALEY	35.3%			
175	ALKDITVYRVNTWHPGVIKTPVDDLGAEAMSQR-TKTPMWHIGEPNDIATIVYLA	35.3%			
180	AAK-GIRVNSVNPQGKTPPLDICP--KEHDYLITQHPIGRLGKPEEIASAVAFLCD	35.3%			
234	ESKFATGSEFVWDDGVTQ	25.2			
236	EATFINGISLVLDDGGTAR	25.4			

Qy	1	MSNRLDGKVNLITGGTGLIGLALATKFVERGAKUMITD-----RHSDVGEKAASKVGTP	54	Length 254;
Qy	1	MSYNFHNKVAVVTGALSGIGLISVAKKFQLOGAKVNTISDVSGEKKYHETVVALKAQNLT-	59	
Qy	55	DQIQFQHDSSEDOGWTKLDETERAFGPVSTLNNAVGAVNKSVVEETTAEWKRLLAVN	114	
Qy	60	DNLHYVQADSKEEDNNKLISSETLATFGGLIDIVCANAGFKFAPTHETIPDWKRVKVAVN	119	
Qy	115	LDGVFGTRGIORMKNGKKGASINMSSIEGVGDPDSLIGAYNASKGAVRIMSKAALDC	174	
Qy	120	LNGVFLDLKAINWLEKSKPGVIVNMGSWHSFVAAPLGAAHYGAKKGGKLLTOTLAEY	179	
Db				5:

(R)-2-octanol dehydrogenase; ketone; alcohol; beta-NAD; co-enzyme; oxidize; optical isomer; (R)-2-octanol; 4-haloacetoacetate ester; (S)-4-halo-3-hydroxybutyrate ester; HMG-CoA reductase inhibitor; D-carnitine; (R)-propoxybenzene.

Pichia finlandica.

WO200161014-A1.

23-AUG-2001.

15-FEB-2001; 2001WO-JP01082.

16-FEB-2000; 2000JP-0043506.

08-DEC-2000; 2000JP-0374593.

(DAIL) DAICEL CHEM IND LTD.

Kudoh M, Yamamoto H;

WPI; 2001-596701/67.

N-PSDB; RAH43472.

(R)-2-octanol dehydrogenase for producing isomers from in 2001082

AC XX
XX AAY56815;
XX
XX DT 31-MAR-2000 (first entry)
XX
DE Bacillus D-arabinitol dehydrogenase
XX D-arabinitol dehydrogenase; clinica
XX OS Bacillus sp.
XX PN JP11332569-A.
XX
PD 07-DEC-1999.
XX
PR 26-MAY-1998; 98JP-0143637.
XX
PR 26-MAY-1998; 98JP-0143637.
PA (IKED-) IKEDA SHOKKEN KK.
PA (NIPK) NIPPON KAYAKU KK.
XX
DR WI; 2000-091353/08.

XX
PT Arabinitol dehydrogenase gene encoding D-arabinitol dehydrogenase
XX useful as a clinical diagnosing agent for mycosis

XX
Claim 1; Page 10-11; 14pp; Japanese.

XX
The invention relates to gene encoding D-arabinitol dehydrogenase,
CC isolated from *Bacillus* sp. IKD-54868 strain. The protein can be expressed
CC by standard recombinant methodologies. D-arabinitol dehydrogenase is used
CC as a clinical diagnosing agent for mycosis. The present sequence
CC represents the D-arabinitol dehydrogenase enzyme.

XX
Sequence 258 AA;

Query Match 31.0%; Score 400; DB 21; Length 258;
Best Local Similarity 39.4%; Pred. No. 1.4e-30; Gaps 7;
Matches 100; Conservative 41; Mismatches 101; Indels 12;

Db 4 RLDGKVAITGGTIGLIGLAIATNFVEGAKVMTDRHSVDGKEKA--KSGVTPDQIOPF 60
8 RLDGKVAITGGTIGLIGLAIATNFVEGAKVMTDRHSVDGKEKA--KSGVTPDQIOPF 60
Oy 61 QHDSSDEDCWTKLFDATKEAFGPVSTLVNNAGIAVAKSVETTAEWRKLAVNLGVF 120
66 QTDVNTDEAQVLEALRQVERQYGRDVLVNAVAGIHKDRAEELPVEWNRMVNVNLSPF 125

Oy 121 GTRIGIORMKNGLGASINMSSIEG-FVGDPs-LGAYNASKGAVRIMSKAALDCALKD 178
126 MSKAAGKVMIRQSKG-SIINISSMSGLIVNTPOPOQAYNVSAGVIMLTKLASEWAP 182

Oy 179 DYVAVNTVHFGYIKPLVDD--LPGAEAMSQRKTPMCHIGEPNDIAYICVYLASNEK 236
183 HGVRVNTVHFGYIKPLVDD--LPGAEAMSQRKTPMCHIGEPNDIAYICVYLASNEK 242

Oy 237 FATGSEFVVDGGYT 250
243 FATGSEFVVDGGYT 256

RESULT 7
ABP38717

ID ABP38717 standard; Protein: 257 AA.

AC ABP38717;

XX
DT 24-JUL-2002 (first entry)

DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3562.

XX
KW Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;

XX
DE Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;

XX
OS Staphylococcus epidermidis.

PN US380370-B1.

XX
PD 30-APR-2002.

XX
PF 13-AUG-1998; 98US-0134001.

PR 14-AUG-1997; 97US-053779P.

PR 08-NOV-1997; 97US-064964P.

XX
PA (GENO-) GENOME THERAPEUTICS CORP.

XX
PI Doucette-Stamm LA, Bush D;

XX
DR WPI; 2002-381255/1.

DR N-PSDB; ABN91262.

XX
Novel isolated nucleic acid encoding a *Staphylococcus epidermidis* polypeptide, useful for diagnosing and treating bacterial infections -

PS Disclosure: SEQ ID 3562; 267PP; English.
XX ABN90538 to ABN93374 represent *Staphylococcus epidermidis* open reading
CC frame (ORF) nucleic acid sequences which encode the amino acid sequences
CC given in ABP3512 to ABP37960. The *S. epidermidis* sequences have
CC antibacterial activity and can be used in gene therapy. The sequences
CC can also be used in the diagnosis and treatment of bacterial infections,
CC particularly *S. epidermidis* infections. The sequences can be used to
CC screen for compounds able to interfere with the *S. epidermidis* life
CC cycle or inhibit *S. epidermidis* infection.
N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the
CC USPTO web site.

XX
SQ Sequence 257 AA;

Query Match 29.1%; Score 376; DB 23; Length 257;
Best Local Similarity 33.7%; Pred. No. 3e-28; Gaps 94; Indels 16;

Db 4 RLDGKVAITGGTIGLIGLAIATNFVEGAKVMTDRHSVDGKEKA--KSGVTPDQIOPF 61
11 KLTGKVAIVMIGGATGIGKAMAELAQAGANIVIADLQSNIGQETTISTQSGWKTSLK 70

Oy 62 HDSSDEDGWTKLFDATKEAFGPVSTLVNNAGIAVAKSVETTAEWRKLAVNLGVF 121
71 LDITHLDENVQIVDVAVREYKGKIDLVNNASISQDDTENISYEWEKLEINLSNGAFSV 130

Db 122 TRIGIORMKNGLGASINMSSIEG-FVGDPs-LGAYNASKGAVRIMSKAALDCALKD 179
131 AQTGVRQMIKSG-SIINISSMSGLIVNTPOPOQAYNVSAGVIMLTKLASEWAP 187

Oy 186 DVRYAVNTVHFGYIKPLVDD--LPGAEAMSQRKTPMCHIGEPNDIAYICVYLASNEK 236
188 GIKVNAIAPGYMT----IETEKILNDNTETNTPMERVGEPEELAGITVYLASNEK 241

Db 237 FATESEFVVDGGYT 251
Oy 242 FTQGSVFNIDGGYS 256

RESULT 8
AAU37095

ID AAU37095 standard; Protein: 272 AA.

XX
AC AAU37095;

XX
DT 14-FEB-2002 (first entry)

DE Staphylococcus aureus cellular proliferation protein #1265.

XX
KW Antisense: prokaryotic cellular proliferation protein;

XX
KW antibiotic; antibacterial; drug design.

OS Staphylococcus aureus.

XX
PN WO200170955-A2.

XX
PD 27-SEP-2001.

XX
PF 21-MAR-2001; 2001WO-US00180.

XX
PR 21-MAR-2000; 2000US-191078P.

PR 23-MAY-2000; 2000US-206848P.

PR 26-MAY-2000; 2000US-207727P.

PR 23-OCT-2000; 2000US-24578P.

PR 27-NOV-2000; 2000US-253625P.

PR 22-DEC-2000; 2000US-257931P.

XX
PR 16-FEB-2001; 2001US-263308P.

XX
PT (ELIT-) ELITRA PHARM INC.

XX
PI Haselbeck R, Ohlsen KJ, Zyskind JW, Wall D, Trawick JD, Carr GJ;

PI	12-OCT-2001.
DR	WPI; 2001-611495/70.
DR	N-FSDB; AASS4954.
XX	
PT	New Polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids -
XX	
PR	Example 3; Seq ID No 12088; 511pp; English.
XX	
CC	The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are <i>Escherichia coli</i> , <i>Staphylococcus aureus</i> , <i>Salmonella typhi</i> , <i>Klebsiella pneumoniae</i> , <i>Pseudomonas aeruginosa</i> and <i>Enterococcus faecalis</i> . The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.
CC	Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences .
CC	
CC	Sequence 272 AA:
XX	
Query	Match 28.6%; Score 369; DB 22; Length 272;
Best	Local Similarity 35.8%; Pred. No. 1.6e-27;
Matches	92; Conservative 42; Mismatches 109; Indels 14; Gaps 6;
QY	4 RLDGKVAAITGGTIGLGLAIAKTFVEEAKVMTDRHSVGEKAAKSVGTPDQIQFQHD 63
Db	3 RLENKVAVVTGASTGQASATALAQEGVAVLAVDIAEAVSETVDKIKNSGDKAKIYVD 62
QY	64 SSDEDQWTKLFDATEKAFGPVSTLNVNAGI-AVNKSVEETTAEWRKLLAVNLDCVFG 121
Db	63 IASEQDQIDNFASEIRSQFGHVQVLNFNNAGVNDNAAGR-IHEYPTDVYDVKIMVDMRTEFLM 121
QY	122 TRLGIGORMKNGLGASITIMSSIEGFVGDPSLGLAYNASKAVRIMSKAALDCALKDYDV 181
Db	122 TKGMMPLMLMK--GGSIVNTSSFSQGQADLYRSGYNAAKGAVINPNTKSAIEYGD-RD-GI 177
QY	182 RVNTVHPGKVTPLVQDPLGABE-----AMSQRTKPMGHICBPNPDIAVIVCLVLASNE 234
Db	178 RANATAPGTEITPLVQDKLGTSEDKEGKAFRENQKWMTPPLGRGKPEEVGKLWVFLASDE 237
QY	235 SKRATGSEFVVDGGYTA 251
Db	238 SSFINGETIRIDGGVVA 254
XX	
SQ	Sequence 272 AA:
XX	
Query	Match 28.5%; Score 368; DB 23; Length 253;
Best	Local Similarity 34.3%; Pred. No. 1.8e-27;
Matches	86; Conservative 48; Mismatches 103; Indels 14; Gaps 4;
QY	8 KVAITNGGTGIGLGLAIAKTFVEEAKVMTDRHSVGEKAAKSVGTPDQIQFQHDSS 67
Db	3 KIAVIGAGOGIGFAALKRKYNGKVAIDYNEBETAQKAKELG--ENSFAIKADVSDR 60
QY	68 DGWTKLFLDATEKAFGPVSTLNVNAGI-AVNKSVEETTAEWRKLLAVNLDCVFG 127
Db	61 EQVISALNAVVDKFGDLNVLVNVNAGIAPTOINTITPQDFHOVWVINVNGGVLWGTSTA 120
QY	128 RMKNGKLGASITIMSSIEGFVGDPSLGLAYNASKAVRIMSKAALDCALKDYDVNTVH 187
Db	121 LFRKGHGKGKINTSQAGVVGPNMLYSSIFAVRGMTQIARD--LAEGITVNA 178
QY	188 PGYKVTPLVDD-----PGAEVAMSQRT--KTPMGHIGERNDIAVIVCLVLASNEF 237
Db	179 PGIVKTPMMEDIAHQVGKNAQKDEWMQTFAKDIAMKRLSEPDVANVNSLAGPSDN 238
QY	238 ATGSEFVVDGG 248
Db	239 ITGQITIVDGG 249
XX	
RESULT	9
ABB54214	AAR2757
ID	AAR2757
XX	
AC	AAR2757
XX	
DE	16-MAY-2002 (first entry)
DE	Lactococcus lactis protein butA.
XX	
KW	Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
OS	Lactococcus lactis IIL403.
XX	
FR	FR2807446-A1.
XX	
RESULT	10
ABB54214	AAR2757
ID	AAR2757
XX	
AC	AAR2757
XX	
DE	11-MAR-1993 (first entry)
DE	Glucose dehydrogenase.
XX	
KW	GDH; mutant; recombinant; mass production; tetramer; thermostable.
OS	Bacillus megaterium.
XX	
FT	Key-Misc-difference 96
FT	Location/Qualifiers
FT	

FT	Misc-difference 252	/note- "site of Gln->Ieu mutation"
FT	Misc-difference 253	/note- "site of Tyr->Glu mutation"
FT	Misc-difference 22	
FT	Misc-difference 43	/label- Ser, Ala
FT	Misc-difference 79	/label- ASP, Glu
FT	Misc-difference 95	/label- Ala, Ser
FT		/label- Leu, Met
PN	JP04258293-A.	OS
XX		XX
XX		Lactobacillus rhamnosus acetoin dehydrogenase butA.
XX		DE
XX		Enzyme; flavour; aroma; texture; nutritional; dairy manufacture; therapy;
XX		fermentation process; anti-infection; rotavirus infection; heart disease;
XX		infantile diarrhoea; lactose digestion; anti-cancer; autoimmune disorder;
XX		KW anti-mutagenesis; immune system modulation; allergy; Helicobacter pylori;
XX		KW anti-hypertensive effect; urogenital infection; hepatic encephalopathy;
XX		KW bowel syndrome; endocarditis; transgenic microbe; acetoin dehydrogenase;
XX		KW butA; EC 1.1.1.5.
XX		XX
XX		Lactobacillus rhamnosus HN001.
XX		XX
PN	W0200212506-A1.	DT
XX		XX
PD	14-FEB-1992.	DE
XX		XX
PF	13-FEB-1991; 91JP-0106927.	DE
XX		XX
PR	13-FEB-1991; 91JP-0106927.	DE
XX		XX
PA	(AMAN) AMANO PHARM KK.	DE
XX		XX
DR	WPI; 1992-354684/43.	DE
XX		XX
PR	Glucose dehydrogenase prep, using transformed recombinant DNA	DE
PT	from <i>Bacillus megaterium</i> - has specified transformations giving	DE
PT	glucose dehydrogenase-expressing vector, introduced into E.coli.	DE
PT	for culture	DE
XX		XX
PS	Claim 1; Page 8; 12pp; Japanese.	XX
XX		XX
CC	The glucose dehydrogenase enzyme is encoded by a recombinant DNA	XX
CC	clone from <i>Bacillus megaterium</i> . The DNA sequence may be mutated by	XX
CC	site-directed mutagenesis to introduce mutations to the protein	XX
CC	sequence (see feature table). The DNA may be used to transform E.	XX
CC	coli cells, and transformants may be cultured to mass produce GDH.	XX
CC	The mutant GDH is not influenced by ion strength, exists as a	XX
CC	tetramer and is thermostable.	XX
SQ	Sequence 261 AA;	XX
Query Match	28.5%; Score 367.5; DB 13; Length 261;	XX
Best Local Similarity	33.3%; Pred. No. 2.1e-27;	XX
Matches	85; Conservative 49; Mismatches 112; Indels 9; Gaps 4;	XX
Oy	1 MSNRDGKVAITGGTIGLGLATKVEGAKVMTIDRHSWDGEKAA---KSVGTPDQ 56	XX
Db	1 MYKDEGKVWVITGGTIGLGLATKVEGAKVMTIDRHSWDGEKAA---KSVGTPDQ 56	XX
Qy	57 IOPFOHDSSDEDGWTKLDEDATEKAFGPVSTLVNNAGIAVANKSVETTAEWKLLAVND 116	XX
Db	59 AIAVKGDVYEVESDVINLYQXIKEFGKGLDVMINNAGXENPVSSHEMSLSDWNKVIDNT 118	XX
Qy	117 GIVFGTRLIGIQRMKNGKLGASINNSISGEVYGDPSLQAGYNAASKGAVIIMSKRALDCAL 176	XX
Db	119 GAFGLSREAIKYFVENDIKGVINMSVHNEKIPPTPLFVHYAASRGGMKLMTEALEYAP 178	XX
Qy	177 KQDVYRNTVHCGYIKPL-VDOLPGAEAMSORTKTMCHIGEPNDVAYICVYLASES 235	XX
Db	179 K--GIRVNVIGPAINTNAEKFADPQRQADYEVESMINGYIGPEEEIAAVAAWLASSEA 236	XX
Qy	236 KFATGSEFWVDDGTY 250	XX
Db	237 SVVTGITLEADGGM 251	XX
SQ	Sequence 261 AA;	XX
Query Match	28.4%; Score 366.5; DB 23; Length 261;	XX
Best Local Similarity	33.5%; Pred. No. 2.6e-27;	XX
Matches	85; Conservative 50; Mismatches 112; Indels 7; Gaps 4;	XX
Oy	1 MSNRDGKVAITGGTIGLGLATKVEGAKVMTIDRHSWDGEKAAKSVGTPDQ 58	XX

Db 1 MYRDLNGKVAVVTTGGSKKGIGAGIAERFGQEHMAYVWVNLGHDHEGARKTADTVIKNGQAV 60
 Qy 59 FFOHDSDEDGWTKLFDATKEKAFGPVSTLVNNAGVTTAENRKLAVNLGV 118
 Db 61 SIHADVSTEAIGLAVLKVKAESGRDWWNNAGMEIKAPTHEVSLDDWWKVIATNQTV 120
 Qy 119 FFGTRIGIQORMKNGKLGASIIINNSIEGFVGDPISLGAYNASKGAVRIMSKSAAALDCALKD 178
 Db 121 FLGARAALNYFLDHQPGNIINISSVHEOIPWPWTFASVAAKGSVLFETIAMEA-N 178
 Qy 179 YDVRVNTVHPGYIKTPVLDLPGAEAMSQRT-KTPMGHICPMDIAYCIVVLASNEK 236
 Db 179 RGIRVNLGPGATE-INAEKFADKAQDQTAVAMIPOGRLGKPEDVAGAAWLASTESS 237
 Qy 237 FATGSEEVFDGGT 250
 Db 238 YVTGTTLFIDGMMT 251

RESULT 12
 AAR04044
 ID AAR0404 standard; protein; 261 AA.
 XX
 AC AAR0404;
 XX
 DT 02-MAR-1993 (first entry)
 XX
 DE Glucose dehydrogenase.
 XX
 KW GDH; vector; E. coli; enzyme; assay; food.
 XX
 OS *Bacillus megaterium*.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 22
 FT /label= SER, ALA
 FT Misc-difference 79
 FT /label= ALA, SER
 FT Misc-difference 95
 FT /label= LEU, MET
 XX
 PN JPO2072878-A.
 XX
 PD 13-MAR-1990.
 XX
 PF 06-SEP-1988; 88JP-0223343.
 PR 06-SEP-1988; 88JP-0223343.
 XX
 PA (AMAN) AMANO PHARM KK.
 XX
 DR WPI: 1990-121044/16.
 XX
 PT Glucose dehydrogenase prodn. from *Bacillus megaterium* - by
 PT culturing recombinant DNA-contg. transformants in nutrient
 culture medium, used in food industry
 PS Claim 1: 12pp; Japanese.

DNA encoding glucose dehydrogenase (GDH) derived from *B. megaterium* encodes the amino acid sequence below. The DNA may be integrated into a vector for replication in *E. coli*. A large amt. of GDH may be produced at low cost. The GDH is used in clinical laboratory tests in the food industry in enzymic assays for glucose determination.

Sequence 261 AA;

Query Match Similarity 28.3%; Score 364.5; DB 11; Length 261; Matches 85; Conservative 49; Mismatches 112; Indels 9; Gaps 4;

Qy 1 MSNRLDGKVAITGTLGIGLAIATKVFEGAKVMTDRHSVGVGKAA--KSVGTPDQ 56
 Db 1 MYKOLEGKVWVITOSSTGKGKXMAIRFATEKAKVWVNRSKEXANSVLEEKVG--GE 58
 Qy 57 IOPFHDSDEDGWTKLFDATKEKAFGPVSTLVNNAGVTTAENRKLAVNLGV 116
 Db 59 AIAVKGDVWVESDVINLYQOSXIKERFGKLQVMINNAGXENPVSHMSLDWNVKVIDTNTL 118
 Qy 117 GIVFGTRIGIQORMKNGKLGASIIINNSIEGFVGDPISLGAYNASKGAVRIMSKSAAALDCAL 176
 Db 119 GARLGSEKAIKFVENDIKGTIVINNSVHEKIPWPLFVHASKGKGMLMTETALEYAP 178
 Qy 177 KYDVRVNTVHPGYIKTPVLDLPGAEAMSQRT-KTPMGHICPMDIAYCIVVLASNE 235
 Db 179 K-GIRVNLGPGAINTPINAKEFADPOERADVEMSMIPMGYIGPEEEIAVAAWLASTESS 236
 Qy 236 KATGSEEVFDGGT 250
 Db 237 SKVTGTTLFIDGMMT 251

RESULT 13
 AAR24018
 ID AAR24018 standard; Protein; 261 AA.
 XX
 AC AAR24018;
 XX
 DT 27-NOV-1992 (first entry)
 XX
 DE Thermostable glucose dehydrogenase from *Bacillus megaterium*.
 XX
 KW Thermostable; increased heat stability; GDH.
 XX
 OS *Bacillus megaterium*.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 22
 FT /label= Ser, Ala
 FT Misc-difference 43
 FT /label= Asp, Glu
 FT Misc-difference 79
 FT /label= Ala, Ser
 FT Misc-difference 95
 FT /label= Leu, Met
 FT Misc-difference 96
 FT /note= "together with residues 252, 253 may be replaced by a thermostability-conferring amino acid provided that taken together they are not Glu, Gln, and Tyr respectively"
 FT Misc-difference 252
 FT /note= "together with residues 96, 253 may be replaced by a thermostability-conferring amino acid provided that taken together they are not Glu, Gln, and Tyr respectively"
 FT Misc-difference 253
 FT /note= "together with residues 96, 252 may be replaced by a thermostability-conferring amino acid provided that taken together they are not Glu, Gln, and Tyr respectively"
 XX
 PN US5114853-A.
 XX
 PD 19-MAY-1992.
 XX
 PF 22-SEP-1989; 89US-0410844.
 XX
 PR 22-SEP-1988; 88JP-0237699.
 XX
 PA (AMAN) AMANO PHARM KK.
 XX
 PI Makino Y, Negoro S, Okada H, Urabe I;
 XX

Glucose dehydrogenase; GlcDH; fusion protein; detection.
Bacillus megaterium.
WO20049039-A2.
24-AUG-2000.
08-FEB-2000; 2000WO-EP00978.
19-FEB-1999; 99DE-1006920.
(MERE) MERCK PATENT GMBH.
Lixweiler W, Burger C, Poeschke O, Hofmann U, Wolf A;
WPI; 2000-558290/51.
NP-PSDB; AAA97948.
Glucose dehydrogenase fusion proteins, useful in expression systems for quick detection of foreign proteins by gel electrophoresis - Disclosure; Page 54-55; 63pp; German.
This invention describes a novel recombinant fusion protein (A) comprising at least a first and a second amino acid sequence, characterized in that the first sequence has the biological activity of a glucose dehydrogenase. Glucose dehydrogenase is useful as a detecto protein (in a detection system) for any type of recombinant protein/polypeptide in a fusion protein. Glucose dehydrogenase can be used to detect protein-protein interactions, where it corresponds to a partner of a recombinant protein/polypeptide. Expression vectors encoding recombinant protein/polypeptide in a recombinant production method. The host cell is also useful for recombinant production of the protein/polypeptide. The fusion proteins containing glucose dehydrogenase can be quickly detected in SDS-PAGE gels. This sequence represents the construction of fusion proteins as described in the method of the invention.
Sequence 272 AA;

Query	Match	28 2%	Score	363.5	DB	21	Length	272
Best Local Similarity	31.5%		Pred.	No. 5.4e-27				
Matches	82;	Conservative		Mismatches	51;	Indels	19;	Gaps
1	MSNRLDGKVAIRTGTLGLGIAATKVFEEGAKVMTN-----DRHSDVGEKAASV	51						
1	WYTDLKDVKWVITGGTGLGRRAAVFQEQEAKVWVINYNEEALDAAKEVEEAGQAT	60						
52	GPRDQIQFOHDSSEDDGWMKLFDATEKAGCPVSTLNNAGAVNKSTETTNEWKLL	111						
61	-----IVQGDYTKKEEDVNLVQTAIKEGTGLDWMNNGAVENPVSHELSLDNWVYK	113						
112	AVNLDCGVEFGTRIGIORMKNKGASINNISIEFGVGDPSLGLAYNASKGAVRMSKSA	171						
114	DNLNTGAGFLGSREAIKYEVENDIKGVINNSVHEMPWPLVHYASKGKLMETIA	173						
172	LCALCKDVKDVRVNMVHPGVIKTPL-VDDLGAEAMSQRTKTPMGHIGEPPNDIAYICVIL	230						
174	LEYAPK-F-GIRVNNIGPGAMNTPINAEKADPEQRADVESIIPMGYIKGPEEEVAAGFL	231						
231	ASNEKSKATGSEFVWDGGT	250						
232	ASQOASVYVTGIFTLEFADGGT	251						

Search completed: April 22, 2003, 17:15:27
Job time : 39 secs

OM protein - protein search, using sw model	Run on: April 22, 2003, 17:14:51 ; Search time 14 Seconds (without alignments)	copyright (c) 1993 - 2003 Compugen Ltd.
Title: US-09-910-033a-2	Sequence: 1 MSNRDQKVAVITGGTGLIG.....NESKFATGSEFVVDGGYTAQ 252	GenCore version 5.1.4.P5-4578
Perfect score: 1290	Scoring table: BLOSUM62	529.613 Million cell updates/sec
Searched: 262574 seqs, 29422922 residues	Gapop 10.0 , Gapext 0.5	
Total number of hits satisfying chosen parameters: 262574	Post-processing: Minimum Match 0%	
Minimum DB seq length: 0	Listing first 45 summaries	
Maximum DB seq length: 200000000		
Pred. No. 1 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		
SUMMARIES		
Result No.	Score	Query Match Length DB ID
1	1277	99.0 252 3 US-08-822-322-8
2	1277	99.0 252 4 US-09-466-103-8
3	1019	79.0 251 3 US-08-822-322-9
4	1019	79.0 251 4 US-09-466-103-9
5	4075.5	31.6 255 4 US-08-815-222-4
6	395.5	30.7 256 4 US-09-504-358-14
7	395.5	30.7 256 4 US-09-954-314-14
8	376	29.1 257 4 US-09-134-001C-3562
9	358.5	27.8 261 4 US-09-468-738B-29
10	358.5	27.8 261 4 US-09-940-019-29
11	348.5	27.0 263 4 US-09-134-001C-4512
12	341	26.4 274 4 US-09-134-001C-4431
13	330.5	25.6 258 4 US-09-504-358-12
14	330.5	25.6 258 4 US-09-954-311-12
15	325	25.2 333 1 US-08-440-856N-4
16	324	25.1 337 1 US-08-440-856A-3
17	319.5	24.8 256 1 US-09-533-188B-7
18	313.5	24.3 290 4 US-09-134-001C-4339
19	312.5	24.2 313 4 US-09-413-814-9
20	308.5	23.9 257 4 US-09-287-097-2
21	307.5	23.8 267 4 US-09-134-001C-5042
22	305	23.6 273 6 5512669
23	302	23.4 262 4 Sequence 6, Appli
24	294	22.8 246 3 US-09-238-481-2
25	22.8	246 4 US-09-572-810A-2
26	293	22.6 246 6 5239279-7
27	291.5	22.6 283 4 US-09-367-012-1
ALIGNMENTS		
RESULT 1	Sequence 8, Application US/08822322	Sequence 1, Appli
US-08-822-322-8	Patent No. 6037158	Sequence 2, Appli
Sequence 8, Application US/08822322	GENERAL INFORMATION:	Sequence 3, Appli
Patent No. 6037158	APPLICANT: Hummel, Werner, Riebel, Bettina	Sequence 4, Appli
GENERAL INFORMATION:	TITLE OF INVENTION: Alcohol dehydrogenase and its use for enzymatic production of chiral hydroxy compounds	Sequence 5, Appli
APPLICANT: Hummel, Werner, Riebel, Bettina	NUMBER OF SEQUENCES: 9	Sequence 6, Appli
TITLE OF INVENTION: alcohol dehydrogenase and its use for enzymatic production of chiral hydroxy compounds	CORRESPONDENCE ADDRESS:	Sequence 7, Appli
NUMBER OF SEQUENCES: 9	ADDRESSEE: Falle & Lynch	Sequence 8, Appli
CORRESPONDENCE ADDRESS:	STREET: 805 Third Avenue	Sequence 9, Appli
ADDRESSEE: Falle & Lynch	CITY: New York City	Sequence 10, Appli
STREET: 805 Third Avenue	STATE: New York	Sequence 11, Appli
CITY: New York City	ZIP: 10022	Sequence 12, Appli
STATE: New York	COUNTRY: USA	Sequence 13, Appli
ZIP: 10022	COUNTRY: USA	Sequence 14, Appli
SEQUENCE DATA:	SEQUENCE DATA:	Sequence 15, Appli
CURRENT APPLICATION DATA:	CURRENT APPLICATION DATA:	Sequence 16, Appli
APPLICATION NUMBER: US/08/822-322	APPLICATION NUMBER: US/08/822-322	Sequence 17, Appli
FILING DATE: 21-March-1997	FILING DATE: 21-March-1997	Sequence 18, Appli
CLASSIFICATION: 435	CLASSIFICATION: 435	Sequence 19, Appli
PRIOR APPLICATION DATA:	PRIOR APPLICATION DATA:	Sequence 20, Appli
APPLICATION NUMBER: DE 196 10 984	APPLICATION NUMBER: DE 196 10 984	Sequence 21, Appli
ATTORNEY/AGENT INFORMATION:	ATTORNEY/AGENT INFORMATION:	Sequence 22, Appli
NAME: Hansson, No. 6037158man D.	NAME: Hansson, No. 6037158man D.	Sequence 23, Appli
REGISTRATION NUMBER: 30,946	REGISTRATION NUMBER: 30,946	Sequence 24, Appli
REFERENCE/DOCKET NUMBER: B00R 1076	REFERENCE/DOCKET NUMBER: B00R 1076	Sequence 25, Appli
TELECOMMUNICATION INFORMATION:	TELECOMMUNICATION INFORMATION:	Sequence 26, Appli
TELEPHONE: (212) 688-9200	TELEPHONE: (212) 688-9200	Sequence 27, Appli
TELEFAX: (212) 838-3884	TELEFAX: (212) 838-3884	Sequence 28, Appli
INFORMATION FOR SEQ ID NO: 8:	INFORMATION FOR SEQ ID NO: 8:	Sequence 29, Appli
SEQUENCE CHARACTERISTICS:	SEQUENCE CHARACTERISTICS:	Sequence 30, Appli
LENGTH: 252 amino acids	LENGTH: 252 amino acids	Sequence 31, Appli
TYPE: amino acid	TYPE: amino acid	Sequence 32, Appli
TOPOLOGY: linear	TOPOLOGY: linear	Sequence 33, Appli
MOLECULE TYPE: protein	MOLECULE TYPE: protein	Sequence 34, Appli
US-08-822-322-8	US-08-822-322-8	Sequence 35, Appli
Query Match	99.0%; Score 1277; DB 3; Length 252;	Sequence 36, Appli
Best Local Similarity	99.0%; Pred. No. 5.7e-129;	Sequence 37, Appli
Matches	0; Mismatches 2; Indels 0; Gaps 0;	Sequence 38, Appli
Sequence 1, Appli	Sequence 39, Appli	Sequence 40, Appli
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Sequence 6, Appli	Sequence 49, Appli	Sequence 50, Appli
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Sequence 8, Appli	Sequence 53, Appli	Sequence 54, Appli
Sequence 9, Appli	Sequence 55, Appli	Sequence 56, Appli
Sequence 10, Appli	Sequence 57, Appli	Sequence 58, Appli
Sequence 11, Appli	Sequence 59, Appli	Sequence 60, Appli
Sequence 12, Appli	Sequence 61, Appli	Sequence 62, Appli
Sequence 13, Appli	Sequence 63, Appli	Sequence 64, Appli
Sequence 14, Appli	Sequence 65, Appli	Sequence 66, Appli
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Sequence 16, Appli	Sequence 69, Appli	Sequence 70, Appli
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Sequence 166, Appli	Sequence 369, Appli	Sequence 370, Appli
Sequence 167, Appli	Sequence 371, Appli	Sequence 372, Appli
Sequence 168, Appli	Sequence 373, Appli	Sequence 374, Appli
Sequence 169, Appli	Sequence 375, Appli	Sequence 376, Appli
Sequence 170, Appli	Sequence 377, Appli	Sequence 378, Appli
Sequence 171, Appli	Sequence 379, Appli	Sequence 380, Appli
Sequence 172, Appli	Sequence 381, Appli	Sequence 382, Appli
Sequence 173, Appli	Sequence 383, Appli	Sequence 384, Appli
Sequence 174, Appli	Sequence 385, Appli	Sequence 386, Appli
Sequence 175, Appli	Sequence 387, Appli	Sequence 388, Appli
Sequence 176, Appli	Sequence 389, Appli	Sequence 390, Appli

RESULT 4
US-09-466-109-9
Sequence 9, Application US/09466109
Patent No. 6225099
GENERAL INFORMATION:
APPLICANT: Hummel, Werner, Riebel, Bettina
TITLE OF INVENTION: Alcohol dehydrogenase and its use for enzymatic production of chiral hydroxy compounds
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felie & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/466, 109
FILING DATE: 17-Dec-1999
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/822, 322
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6225099man D.
REGISTRATION NUMBER: 30, 946
REFERENCE/DOCKET NUMBER: BOER 1076
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-466-109-9

Query Match 79.0%; Score 1019; DB 4; Length 251;
Best Local Similarity 80.5%; Pred. No. 2.8e-101; Mismatches 35; Indels 0; Gaps 0;
Matches 202; Conservative 14; Mi smatches 35; Indels 0; Gaps 0;

QY 2 SNRLDGKVATITGGTGLGGLAIAATKFVERGAKVMTIDRHSVGEKAASKGTGPDQIOPFO 61
Db 1 TDLRKGVAVAVGGTGLGGLAIAADKFVERGAKVITGRHADVGKEXXXXXX 60

QY 62 HDSSDEGWTKLFDATEKAFGPVSTLVNNAGIAYNKSVEETTAEMRKLLAVNLDCVFFG 121
Db 61 XXXXXXXXXXXXXLFDATEKAFGPVSTLVNNAGIAYNKSVEETTAEMRKLLAVNLDCVFFG 120

QY 122 TRLGQRMKNGKLGASITIMSSIEFGVFGDPSLGYNASGAVRIMSKSAALDCALKDYD 181
Db 121 TRLGQAMKXGIGASTINMSSTEGFVGDPSLGYNASGAVRIMSKSAALDCALKDYD 180

QY 182 RVNTVHGYIKPLVDDLGAEAMSQRTKPMGHIGERNDIAYICVYLASNEKFATGS 241
181 RVNTVHGYIKPLVDDLGAEAMSQRTKPMGHIGERNDIAYICVYLASNEKFATGS 240

RESULT 5
US-08-815-225-4
Sequence 4, Application US/08815225
Patent No. 628479
GENERAL INFORMATION:
APPLICANT: Stern, David M.
APPLICANT: Yan, Shi Du
TITLE OF INVENTION: AN INTRACELLULAR AMYLOID-BETA PEPTIDE
TITLE OF INVENTION: BINDING (ERAB) POLYPEPTIDE AND METHODS FOR INHIBITING
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS-MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815, 225
FILING DATE: 12-MAR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28, 678
REFERENCE/DOCKET NUMBER: 0575/55209
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-815-225-4

Query Match 31.6%; Score 407.5; DB 4; Length 255;
Best Local Similarity 39.0%; Pred. No. 1.2e-35; Mismatches 103; Indels 7; Gaps 5;
Matches 97; Conservative 42; Mi smatches 35; Indels 7; Gaps 5;

QY 3 NRLDGKVATITGGTGLGGLAIAATKFVERGAKVMTIDRHSVGEKAASKGTGPDQIOPFO 62
Db 2 NDLSGKVATITGGTGLGGLAIAARQAVAGARVVLADVLDEEGATAREG-DARYQH 59

QY 63 DSSDEGWTKLFDATEKAFGPVSTLVNNAGIAYNKSVEETTAEMRKLLAVNLDCVFFG 122
Db 60 DVIIEEDWQRVVAAREFGSVDLGVNNAGIYSGMFLETESVRRKVDINLTOVFIGM 119

QY 123 RLGIQRMKNGKLGASITIMSSIEFGVGDPSLGYNASGAVRIMSKSAALDCALKDYD 182
Db 120 KTVIPAMKDAG-GSTGVNISSAAGLMLALTSSYQASKWVGRLSKLAAVE-LGTDRI 176

QY 183 VNTVHGYIKPLVDDLGAEAMSQRTKPMGHIG-EPNDIAYICVYLASNEKFATGS 241
Db 177 VNSVHGMGTYRPTMAE-TGIGQEGEYNPNTPMGRVGNRGEIGAIVAWKLSDISSYVTGA 235

QY 242 EFVDDGTY 250
Db 236 ELAVDGGT 244

RESULT 6
 US-09-504-358-14
 Sequence 14, Application US/09504358
 Patent No. 636376
 GENERAL INFORMATION:
 APPLICANT: Roviere, Pierre E.
 TITLE OF INVENTION: GENES AND ENZYMES FOR THE PRODUCTION OF ADIPIC ACID INTERMEDIATES
 FILE REFERENCE: BC1001 US NA
 CURRENT APPLICATION NUMBER: US/09/504, 358
 CURRENT FILING DATE: 2000-02-15
 EARLIER APPLICATION NUMBER: 60/120,702
 EARLIER FILING DATE: 1999-February-19
 NUMBER OF SEQ ID NOS: 49
 SOFTWARE: Microsoft Office 97
 SEQ ID NO 14
 LENGTH: 256
 TYPE: PRT
 ORGANISM: *Brevibacterium* sp HCU
 US-09-504-358-14

Query Match 30.7%; Score 395.5; DB 4; Length 256;

Best Local Similarity 37.7%; Pred. No. 2.3e-34; Mismatches 104; Indels 15; Gaps 6; Matches 98; Conservative 43; Mismatches 104; Indels 15; Gaps 6;

Qy 3 NRLDKKAVAITGGTGLGIGLATAKFKVEGAKWMTDRHSVGEKAASKVGTPOQ-I-QFQ 61
 Db 2 NRLGKGVAVITGGTGLGIGLATAKFKVEGAKWMTDRHSVGEKAASKVGTPOQ-I-QFQ 61

Qy 52 HDSSDEGWTKLFDATEKAFFGPPVSTLVNNAGT-AVNKSVEETTAEWRKLLAVNLGVFF 120
 Db 62 LDVSDSEVEIWSDIKRFGA,INVLVNNAGT-IGADPKPHEIDERDLDLVLSVLKVGF 121

Qy 121 GTRLGIGRMKNGLGASINMSIEGFVGDPSPGAYNNSKGAVRIMSKSAAALCALDKD 180
 Db 122 MYKHCIPYFKQAG-GGATVNFASVYGLVGSQELTPYHAKGVWALTKDQAV-TYGSN 178

Qy 181 VRVNTVHGYIPLV-----DPLGAEEAMSQRKTPMCHIGEPNDIAYCVYLAS 232
 Db 179 IRVNAVAPGTTPLVKELGSGSPGDLGDTYKLMG-AKHPGLGRVTPPEEVAAFLAS 236

Qy 233 NESKFAKGSEFWVDDGGYTAQ 252
 Db 237 EEARSTFGAVLIVDGGYTAQ 256

RESULT 8
 US-09-134-001C-3562

; Sequence 3562, Application US/09134001C
 ; Patent No. 6360370
 GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: GICC-007

CURRENT APPLICATION NUMBER: US/09/134-001C
 CURRENT FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: US 60/064, 964

PRIOR FILING DATE: 1997-11-08
 PRIOR APPLICATION NUMBER: US 60/055, 779

PRIOR FILING DATE: 1997-08-14
 NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 3562
 LENGTH: 257

TYPE: PRT
 ORGANISM: *Staphylococcus epidermidis*

US-09-134-001C-3562

Query Match 29.1%; Score 376; DB 4; Length 257;

Best Local Similarity 33.7%; Pred. No. 2.8e-32; Mismatches 94; Indels 16; Gaps 6; Matches 86; Conservative 59; Mismatches 94; Indels 16; Gaps 6;

Qy 14 Application US/09954314

SEQUENCE 14, Application US/09954314

PATENT NO. 6465224

GENERAL INFORMATION:

APPLICANT: Roviere, Pierre E.

APPLICANT: Roviere, Pierre E.

APPLICANT: Birostowicz, Patricia C.

TITLE OF INVENTION: GENES AND ENZYMES FOR THE PRODUCTION OF ADIPIC ACID INTERMEDIATES

FILE REFERENCE: BC1001 US NA

CURRENT APPLICATION NUMBER: US/09/504, 314

CURRENT FILING DATE: 2001-09-17

PRIOR APPLICATION NUMBER: 60/120,702

PRIOR FILING DATE: 1999-February-19

NUMBER OF SEQ ID NOS: 49

SOFTWARE: Microsoft Office 97

SEQ ID NO 14

LENGTH: 256

TYPE: PRT

ORGANISM: *Brevibacterium* sp HCU

US-09-504-314-14

Query Match 30.7%; Score 395.5; DB 4; Length 256;

Best Local Similarity 37.7%; Pred. No. 2.3e-34; Mismatches 98; Conservative 43; Mismatches 104; Indels 15; Gaps 6;

Qy 3 NRDGKGVAVITGGTGLGIGLATAKFKVEGAKWMTDRHSVGEKAASKVGTPOQ-I-QFQ 61
 Db 11 KLTGKGVAVITGGTGLGIGLATAKFKVEGAKWMTDRHSVGEKAASKVGTPOQ-I-QFQ 61

Qy 62 HDSSDEGWTKLFDATEKAFFGPPVSTLVNNAGT-AVNKSVEETTAEWRKLLAVNLGVFF 120
 Db 71 LDITHLDENVQIVDVKVREYKGKIDILVNNASISQDDTENTISYEENLKEINLNSGAFV 130

Qy 122 TRIGIORMKNGLGASINMSIEGFVGDSS-LGAYNASKGAVRIMSKSAAALCALDKD 179
 Db 131 AQTVGROMTEKGSG-SMINYSSVGLIANKHODQSYETSRRGVTMLTKSULARES-RY 187

Qy 180 VRVNTVHGYIPLVLDLUI-EGAEAMSQRK---TPMGHIGEPNDIAYCVYLASNEK 236
 Db 188 GIKVNAIAGYMT-----IETEKILNDNTETNT'PMERGEPEBLAGTVYLASDASS 241

Qy 237 FATOSEFVVDGGYTAQ 251
 Db 242 FTQGSVFNIDGGYSA 256

RESULT 9

US-09-468-738A-29

; Sequence 29, Application US/09468738A

; Patent No. 6312933

GENERAL INFORMATION:

APPLICANT: Kimoto, No. 6312933

APPLICANT: Yamamoto, Hiroaki

APPLICANT: Mitsuhashi, Kazuya
 TITLE OF INVENTION: NOVEL CARBONYL REDUCTASE, METHOD FOR PRODUCING SAID ENZYME, AND METHOD FOR PRODUCING ALCOHOL USING SAID ENZYME
 FILE REFERENCE: 06501-050001
 CURRENT APPLICATION NUMBER: US/09/468,738A
 CURRENT FILING DATE: 1999-12-21
 PRIORITY APPLICATION NUMBER: JP 1999-171160
 PRIORITY FILING DATE: 1999-06-17
 PRIORITY APPLICATION NUMBER: JP 1998-363130
 PRIORITY FILING DATE: 1998-12-21
 SOFTWARE: PatentIn Ver. 2.0, reformatted using WordPerfect 5.1
 SEQ ID NO: 29
 LENGTH: 261
 TYPE: PRT
 ORGANISM: *Bacillus subtilis*
 US-09-468-738A-29

Query Match 27.8%; Score 358.5; DB 4; Length 261;
 Best Local Similarity 33.9%; Pred. No. 2.2e-10; Mismatches 104; Indels 21; Gaps 5;
 Matches 87; Conservative 45; MisMatches 104; Indels 21; Gaps 5;

QY 5 LDGKVAITTGTCIGLIAATKVEEGAKVMIT---DRHSVGEKAQSKVTPDQIQF 59
 Db 5 LKGKVVAITGAASGLGKAMAIRFGKEQAKVYINYNSNKQDPNEKVKEVKG---EAVV 61

QY 60 FQHDSSEDEGWTKLDATEKAFFGPVSTLVNNAGIAVNKSVEETTAEWRKLLAVNLGVF 119
 Db 62 VQGDVYKEEDVKNVQTAKEFGTLDINNNAGLENPVPSHEMLKDVKVGTNTGAF 121

QY 120 FGTRLGIORMNKKGAGASINMSSEGFDPSLGRAYNASKGAVRIMSKSAALDCALDGY 179
 Db 122 LGSRRAIKYFVENDIKGNVINMSSHEVIEPMLFVHIAASKKGIKLMETLALEYAPK-- 179

QY 180 DWRVNTVPGYIKPLVLDLPGAEAMQRTK---PMGHIGEPNDIAYCVYLASN 233
 Db 180 GIRVNNICPGAINNPI---NAEKFADPKKADVESMPMGYIGEPEEIAAVAAWLAST 234

QY 234 ESKPATGSEFVVDGGYT 250
 Db 235 EASYVTGCTLFADGGMT 251

RESULT 10
 US-09-940-019-29
 ; Sequence 29, Application US/09940019
 ; Patent No. 6416986

; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCCUS
 ; FILE REFERENCE: GTC-001C
 ; CURRENT APPLICATION NUMBER: US/09/134,001C
 ; CURRENT FILING DATE: 1998-08-13
 ; PRIORITY APPLICATION NUMBER: US 60/064,964
 ; PRIORITY FILING DATE: 1997-11-08
 ; PRIORITY APPLICATION NUMBER: US 60/055,779
 ; PRIORITY FILING DATE: 1997-08-14
 ; NUMBER OF SEQ ID NOS: 5674
 ; SEQ ID NO: 4512
 ; LENGTH: 263
 ; TYPE: PRT
 ; ORGANISM: *Staphylococcus epidermidis*
 US-09-134-001C-4512

Query Match 27.0%; Score 348.5; DB 4; Length 263;
 Best Local Similarity 31.0%; Pred. No. 2.6e-29; Mismatches 100; Indels 19; Gaps 4;
 Matches 79; Conservative 57; MisMatches 100; Indels 19; Gaps 4;

QY 8 KVAITGGTCIGLIAATKVEGAKVMTDRHSVGEKAQSKVTPDQ-IQFQHDS 66
 Db 10 KVAITGGTCIGLIAATKVEGAKVMTDRHSVGEKAQSKVTPDQ-IQFQHDS 69

QY 67 EDCWTKLDATEKAFFGPVSTLVNNAGIAVNKSVEETTAEWRKLLAVNLGVF 126
 Db 70 RDOVFSVIMQVVEHFDIINLYNNAGLCPMTPIESVPEPQFNOVVGUVGGVFWGIQAI 129

QY 127 QRMKNGKGAGASINMSSEGFDPSLGRAYNASKGAVRIMSKSAALDCALDGY 186
 Db 130 EDFDKLGHGKINNATSOAGVEGNAGLSSYSSKFAVRGLTOAARDLAEK--NITVNAF 187

QY 187 HPIYIKPLVLDLPGAEAMQRTKTPM-----GHIQEPNDIAYCVYLASN 233
 Db 188 ASGIVIPEPM--MKGIKEKLAENNQPMNEWGNQKFTDOIALKRLSKPFDVANV/FLAGS 244

QY 234 ESKPATGSEFVVDGG 248
 Db 245 DSDYITGOTIIVDGG 259

RESULT 11
 US-09-134-001C-4512
 ; Sequence 4431, Application US/09134001C
 ; Patent No. 6380370

RESULT 12

Query Match 27.8%; Score 358.5; DB 4; Length 261;
 Best Local Similarity 33.9%; Pred. No. 2.2e-30; Mismatches 104; Indels 21; Gaps 5;
 Matches 87; Conservative 45; MisMatches 104; Indels 21; Gaps 5;

GENERAL INFORMATION:
 APPLICANT: Lynn Doucette-Stamm et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 FILE REFERENCE: GTC-007
 CURRENT APPLICATION NUMBER: US/09/134,001C
 CURRENT FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: US 60/064,964
 PRIOR APPLICATION NUMBER: US 60/055,779
 NUMBER OF SEQ ID NOS: 5674
 SEQ ID NO 4431
 LENGTH: 274
 TYPE: PRT
 ORGANISM: *Staphylococcus epidermidis*
 US-09-134-001C-4431

Query Match

Best Local Similarity 26.4%; Score 341; DB 4; Length 274;

Matches 88; Conservative 49; Mismatches 106; Indels 14; Gaps 7;

Qy

Db

QY 241 SERVDDGGTYAQ 252

RESULT 2

; Sequence 2, Application US/09978758-2
; Publication No. US20020192783A1
; GENERAL INFORMATION:
; APPLICANT: Kudo, Masatake
; APPLICANT: Yamamoto, Hiroaki
; TITLE OF INVENTION: (R)-2-OCTANOL DEHYDROGENASES, METHODS
; TITLE OF INVENTION: FOR PRODUCING THE ENZYMES, DNA ENCODING THE ENZYMES, AND
; FILE REFERENCE: 06501-090001
; CURRENT APPLICATION NUMBER: US/09/978,758
; CURRENT FILING DATE: 2002-04-19
; PRIORITY APPLICATION NUMBER: PCT/JP01/01082
; PRIORITY FILING DATE: 2001-02-15
; PRIORITY APPLICATION NUMBER: JP 2000-374593
; PRIORITY FILING DATE: 2000-12-08
; PRIORITY APPLICATION NUMBER: JP 2000-43506
; PRIORITY FILING DATE: 2000-02-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Pichia finlandica
; US-09-978-758-2

Query Match 32.5%; Score 419; DB 10; Length 253;
Best Local Similarity 39.1%; Pred. No. 9.1e-32; Mismatches 103; Indels 6; Gaps 4;
Matches 97; Conservatve 42; Mismatches 103; Indels 6; Gaps 4;

QY 3 NRLDCKVAVITGGTIGLIGLAIATKVEEGAKVMDIDRHSVDGEGAKAAGKSVGPPDQIOFFQH 62
Db 1 NDLSCKTVITGGGARGLGAEARQAVAGRKVLLDVLDEGAATARELG--DAARYOHL 58

QY 63 DSSDIDGWTKLFDATETKAFCGPVSTIYNNAGAVNSVEETTAERKLLAVNLDSVFFGT 122
Db 59 DVTBEDWQRYVAYAREEFGSDVQYNNAGISTGMPLETESVERRKYVETNLTQVFIGM 118

QY 123 RLGGQRMKNGLGLASSINMSIEGVGDPGSLGAYVASKGAVRIMSKSAALDCALADYDVR 182
Db 119 KTVIPAMKAG-GOSIINNSAAGLMTSSYKASKWVGRGSKLAVAE--LGDTRR 175

QY 183 VNTVHPGYLKTPLVDDPLGAEEAMSQRTKPMGHGEPNDIAYTCVYLASNESKTGSE 242
Db 176 VNSPHPGMVYTPMVAE-TGIRQEGCENYPPNTPMGRVGEPEIAGAVVKLISDTSSVIGAE 234

QY 243 FVVDGGYT 250
Db 235 LAVDGGWT 242

RESULT 3

; Sequence 3, Application US/09931186
; Patent No. US20020132319A1
; GENERAL INFORMATION:
; APPLICANT: ABREO, MELWYN A.
; APPLICANT: AGRE, CHARLES S.
; APPLICANT: AUST, ROBERT
; APPLICANT: KISSINGER, CHARLES R.
; APPLICANT: MARGOSIAK, STEVE
; APPLICANT: MENG, JERRY J.
; APPLICANT: PELLETIER, LAURA A.
; APPLICANT: REJTO, PAUL A.
; APPLICANT: SHOMALTER, RICHARD E.
; APPLICANT: TEMOCZYK, RUSSELL, ANNA
; APPLICANT: THOMSON, JIM

QY 09-931-186-15
; Sequence 15, Application US/09931186
; Patent No. US20020132319A1
; GENERAL INFORMATION:
; APPLICANT: ABREO, MELWYN A.
; APPLICANT: AGRE, CHARLES S.
; APPLICANT: AUST, ROBERT
; APPLICANT: KISSINGER, CHARLES R.
; APPLICANT: MARGOSIAK, STEVE
; APPLICANT: MENG, JERRY J.
; APPLICANT: PELLETIER, LAURA A.
; APPLICANT: REJTO, PAUL A.
; APPLICANT: SHOMALTER, RICHARD E.
; APPLICANT: TEMOCZYK, RUSSELL, ANNA
; APPLICANT: THOMSON, JIM

QY 09-931-186-15
; Sequence 15, Application US/09931186
; Patent No. US20020132319A1
; GENERAL INFORMATION:
; APPLICANT: VANDERPOOL, DARIN
; APPLICANT: VILLARANCA, J. ERNEST
; TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
; TITLE OF INVENTION: STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
; TITLE OF INVENTION: OF INHIBITORS THEREOF
; FILE REFERENCE: 0125-0049
; CURRENT APPLICATION NUMBER: US/09/931,186
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Steptomyces hydrogenans
; US-09-931-186-15

Query Match 32.5%; Score 419; DB 10; Length 253;
Best Local Similarity 39.1%; Pred. No. 9.1e-32; Mismatches 103; Indels 6; Gaps 4;
Matches 97; Conservatve 42; Mismatches 103; Indels 6; Gaps 4;

QY 3 NRLDCKVAVITGGTIGLIGLAIATKVEEGAKVMDIDRHSVDGEGAKAAGKSVGPPDQIOFFQH 62
Db 1 NDLSCKTVITGGGARGLGAEARQAVAGRKVLLDVLDEGAATARELG--DAARYOHL 58

QY 63 DSSDIDGWTKLFDATETKAFCGPVSTIYNNAGAVNSVEETTAERKLLAVNLDSVFFGT 122
Db 59 DVTBEDWQRYVAYAREEFGSDVQYNNAGISTGMPLETESVERRKYVETNLTQVFIGM 118

QY 123 RLGGQRMKNGLGLASSINMSIEGVGDPGSLGAYVASKGAVRIMSKSAALDCALADYDVR 182
Db 119 KTVIPAMKAG-GOSIINNSAAGLMTSSYKASKWVGRGSKLAVAE--LGDTRR 175

QY 183 VNTVHPGYLKTPLVDDPLGAEEAMSQRTKPMGHGEPNDIAYTCVYLASNESKTGSE 242
Db 176 VNSPHPGMVYTPMVAE-TGIRQEGCENYPPNTPMGRVGEPEIAGAVVKLISDTSSVIGAE 234

QY 243 FVVDGGYT 250
Db 235 LAVDGGWT 242

RESULT 4

; Sequence 4, Application US/09954314
; Patent No. US20020127666A1
; GENERAL INFORMATION:
; APPLICANT: Rouvire, Pierre E.
; APPLICANT: Brzostowicz, Patricia C.
; TITLE OF INVENTION: GENES, AND ENZYMES FOR THE PRODUCTION OF ADIPIC ACID: INTERMEDIATES
; FILE REFERENCE: BC1001 US NA
; CURRENT APPLICATION NUMBER: US/09/954,314
; CURRENT FILING DATE: 2001-09-17
; PRIORITY APPLICATION NUMBER: 60/120,702
; PRIORITY FILING DATE: 1999-February-19
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 14
; LENGTH: 256
; TYPE: PRT
; ORGANISM: brevibacterium sp HCU
; US-09-954-314-14

Query Match 30.7%; Score 395.5; DB 10; Length 256;
Best Local Similarity 37.7%; Pred. No. 1.5e-29;
Matches 98; Conservatve 43; Mismatches 104; Indels 15; Gaps 6;
Matches 98; Conservatve 43; Mismatches 104; Indels 15; Gaps 6;

QY 3 NRLDCKVAVITGGTIGLIGLAIATKVEEGAKVMDIDRHSVDGEGAKAAGKSVGPPDQIOFFQ 61
Db 2 NRLLGGKVAVITGGAGMGRQISQELASBGAVAVVQNEOGRATADAIRASGVANWKR 61

QY 62 HDSSEDQWTKLEDATEKAFGPVSTIYNNAGI--AVNSVEETTAERKLLAVNLDSVFF 120
Db 62 LDVSDDEBEVIVSDIKRFGAIVLNVYIAGVAKPHEPDKPHTDPRDPLVSVNWKYCR 121

QY 121 GTRGIQIORMKNGLGLASININMSSIEGVGDPGSLGAYNASKGAVRIMSKAALDCALKDYD 180
 ; | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 122 MTKHICIPYFKQAG-GGAIVNFAISIYGLVGSQELTPYHAKGAVVALKTQDAV-TYGPSN 178
 QY 181 VRVWVHPGVIKTPLY-----DDUPGAEBAMSQRKTPMGHIGEPNDIAYICVYLAS 232
 ; | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 179 IRVNVAAPGTLTLPVKELGSRGPDGLDGYTLMG-AKHPPLGRVGTPEEEVAATLFLAS 236
 ; | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 ; Sequence 12688, Application US/09815242
 ; Patent No. US20020159976A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari L.
 ; APPLICANT: Zyskind, Judith W.
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John D.
 ; APPLICANT: Carr, Grant J.
 ; APPLICANT: Yamamoto, Robert T.
 ; TITLE OF INVENTION: Identification of Essential Genes in
 ; TITLE OF INVENTION: Prokaroytes
 ; FILE REFERENCE: ELITRA_011A
 ; CURRENT APPLICATION NUMBER: US/09/815,242
 ; CURRENT FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; NUMBER OF SEQ ID NOS: 14110
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 12688
 ; LENGTH: 272
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 ; US-09-815-22-12688

Query Match 28.6%; Score 369; DB 10; Length 272;
 Best Local Similarity 35.8%; Pred. No. 5.1e-27;
 Matches 92; Conservative 42; Mismatches 109; Indels 14; Gaps 6;

QY 4 RLDGKVALITGGTGLGIAINTKVEGAKVMT--DRHSDVGEKAASKVGTPOIQ 58
 ; | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 3 RLENKVAVWVGASTGIGQASAIALADBEAGVYLAVDIAEAVSETWDKIKSGDKAKVVD 62
 ; | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 QY 64 SSDEERGWTKEFDATEKAFGPVSTLVLNAGI--AVNKSVEETTAEWRKLLAVNLDGVFFG 181
 ; | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 63 IASEQDQINPASEIRQFGHDFVLNNAGVDNAGR-THEPVYDVKIMNDMRGTFLM 121
 ; | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 QY 122 TRLGJORMKNGLGLASININMSSIEGVGDPGSLGAYNASKGAVRIMSKAALDCALKDYD 181
 ; | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 122 TKMMPPLMMTK--GSIVNVISSFSFGQADLYKNSGYNARKGAVINTFKSIAIEG-RD-GI 177
 ; | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 QY 182 RVNTVHPGYIKTPVLDLPGAE-----AMSORTKPMPGIGEPNDIAYICVYLASNE 234
 ; | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 178 RANAIAPGTIEMPLVOKLGTSEDEKEKAFRENIQKWMPLGRLGKPEEEVGKLVFLASDE 237
 ; | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 5
 US-09-815-242-12688
 ; Sequence 12688, Application US/09815242
 ; Patent No. US20020159976A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Glenn, Matthew
 ; APPLICANT: Havukka, Tirkka
 ; APPLICANT: Blohsberg, Leonard
 ; APPLICANT: Lubbers, Mark
 ; APPLICANT: Dekker, James
 ; APPLICANT: Christensson, Anna
 ; APPLICANT: Holland, Ross
 ; APPLICANT: O'Toole, Paul
 ; APPLICANT: Reid, Julian
 ; APPLICANT: Coolbear, Timothy
 ; TITLE OF INVENTION: Lactobacillus rhamnosus Polynucleotides, Polypeptides and Me
 ; TITLE OF INVENTION: Using Them
 ; FILE REFERENCE: 10432
 ; CURRENT APPLICATION NUMBER: US/09/971,536
 ; CURRENT FILING DATE: 2001-10-02
 ; PRIOR APPLICATION NUMBER: U.S. No. US20020159976A1 09/634,238
 ; PRIOR FILING DATE: 2000-08-08
 ; PRIOR APPLICATION NUMBER: U.S. No. US20020159976A1 09/724,623
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: PCT/NZ01/00160
 ; PRIOR FILING DATE: 2001-08-08
 ; PRIOR APPLICATION NUMBER: PCT/NZ01/00160
 ; NUMBER OF SEQ ID NOS: 83
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 74
 ; LENGTH: 261
 ; TYPE: PRT
 ; ORGANISM: Lactobacillus rhamnosus
 ; US-09-971-536-74

Query Match 28.4%; Score 366.5; DB 9; Length 261;
 Best Local Similarity 33.5%; Pred. No. 8.2e-27;
 Matches 85; Conservative 50; Mismatches 112; Indels 7; Gaps 4;

QY 1 MSNRLDGKVALITGGTGLGIAINTKVEGAKVMT--DRHSDVGEKAASKVGTPOIQ 58
 ; | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 1 MYRDLNGKVAVTGGSKGKGIGAGIARFQGEHMAVINYLDHEGARKTADTVKNGQAV 60
 ; | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 QY 59 FFQHSSDEDGWTKLFDATBKAFGPVSTLYNNAGVNKSVEETTAEWRKLLAVNLDGV 118
 ; | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 61 SIHADSVPEFAGIASLVKTESEGRDLYWNNAGHEIKAPTHEVSUDDWNRVIAINTGV 178
 ; | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 QY 119 FFGTRGLIORMKNGLGLASININMSSIEGVGDPGSLGAYNASKGAVRIMSKAALDCALKDYD 178
 ; | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 121 FLGARAALNLYFLDHQPGNINISSYHEQDPMPTASYRAAKGSVLFETIAMEA-N 178
 ; | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 QY 179 YDVRVNTVHPGYIKTPVLDLPGAEAMSORT--KPMGHIGEPNDIAYICVYLASNE 236
 ; | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 179 RGIRVNAIAGPGATEIP-INAEKFADKAQYDQTVAMIPQGRLGKPEEDVAAGMALLTSS 237
 ; | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 QY 237 FAYGSEFVYDGGYT 250
 ; | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 238 YVNGTTLFIDGGMT 251
 ; | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 ; Sequence 589, Application US/09815242
 ; Patent No. US20020159976A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari L.
 ; APPLICANT: Zyskind, Judith W.

RESULT 6
 US-09-971-536-74
 ; Sequence 74, Application US/09971536
 ; Patent No. US20020159976A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Reid, Julian
 ; APPLICANT: Coolbear, Timothy
 ; TITLE OF INVENTION: Lactobacillus rhamnosus Polynucleotides, Polypeptides and Me
 ; TITLE OF INVENTION: Using Them
 ; FILE REFERENCE: 10432
 ; CURRENT APPLICATION NUMBER: US/09/971,536
 ; CURRENT FILING DATE: 2001-10-02
 ; PRIOR APPLICATION NUMBER: U.S. No. US20020159976A1 09/634,238
 ; PRIOR FILING DATE: 2000-08-08
 ; PRIOR APPLICATION NUMBER: U.S. No. US20020159976A1 09/724,623
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: PCT/NZ01/00160
 ; PRIOR FILING DATE: 2001-08-08
 ; PRIOR APPLICATION NUMBER: PCT/NZ01/00160
 ; NUMBER OF SEQ ID NOS: 83
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 74
 ; LENGTH: 261
 ; TYPE: PRT
 ; ORGANISM: Lactobacillus rhamnosus
 ; US-09-971-536-74

APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John D.
 APPLICANT: Carr, Grant J.
 APPLICANT: Yamamoto, Robert T.
 APPLICANT: Xu, H. Howard
 TITLE OF INVENTION: Identification of Essential Genes in
 FILE REFERENCE: ELTRA.011A
 CURRENT APPLICATION NUMBER: US/09/815,242
 CURRENT FILING DATE: 2001-03-21
 PRIORITY APPLICATION NUMBER: 60/191,078
 PRIORITY FILING DATE: 2000-03-21
 PRIORITY APPLICATION NUMBER: 60/206,848
 PRIORITY FILING DATE: 2000-05-23
 PRIORITY APPLICATION NUMBER: 60/207,727
 PRIORITY FILING DATE: 2000-05-26
 PRIORITY APPLICATION NUMBER: 60/242,578
 PRIORITY FILING DATE: 2000-10-23
 PRIORITY APPLICATION NUMBER: 60/253,625
 PRIORITY FILING DATE: 2000-11-27
 PRIORITY APPLICATION NUMBER: 60/257,931
 PRIORITY FILING DATE: 2000-12-22
 PRIORITY APPLICATION NUMBER: 60/269,308
 PRIORITY FILING DATE: 2001-02-16
 NUMBER OF SEQ ID NOS: 14110
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 5689
 LENGTH: 251
 TYPE: PRT
 ORGANISM: *Staphylococcus aureus*
 US-09-815-242-5689

Query Match 27.8%; Score 358.5; DB 10; Length 261;
 Best Local Similarity 33.9%; Pred. No. 4.7e-26;
 Matches 87; Conservative 45; Mismatches 106; Indels 21; Gaps 5;

Qy 5 LDGKVAITGGLGIGLAIATKVEVERGAKWMTDRHSDVGEKAASKVGTPDQIOFFQHDS 64
 Db 1 LENKVAVTGAGSTGIGAAILAQEGAVLAVDIAEVSETVDKIKNGDAKAVVNDI 60

Qy 65 SDEQGWTKLFDATEKAAGPVSTLVNNAGI--AVNKSVEETTAEWKLLAVNLGFF 122
 Db 61 ASEQIDINPASEIRBQFHVDFVLNNAGVNDIAGR-THEPTDVDKIMNDMRTGFLMT 119

Qy 123 RLGIGTORMKNGLGASIIINMSIEGPGDLSGAYNASKGAVRIMKSALDCALKDYDVR 182
 Db 120 KMMPLMWTK-GGSIVNTTSSFGQAAQADLYRSRGYNAKGAVINFTKSIALEYG-RD-GIR 175

Qy 183 VNTVHPGKIKTPDVLPGAAE----AMSQRTKTPMCHIGERNDIATIVYLASES 235
 Db 176 ANATPGVTTPLVQDPLKLTGTSDEKGAFRENQKWTPLGRGKPEENGKLVFLASDES 235

Qy 236 KFATGSEFVDDGGTA 251
 Db 236 SFTGETVRIDGGVMA 251

RESULT 9
 US-09-815-242-11860
 Sequence 11860, Application US/09815242
 Patent No. US2002061569A1
 GENERAL INFORMATION:
 APPLICANT: Hasebeck, Robert
 APPLICANT: Ohlsen, Kari L.
 APPLICANT: Zyskind, Judith W.
 APPLICANT: Wall, Daniel
 APPLICANT: Carr, Grant J.
 APPLICANT: Yamamoto, Robert T.
 APPLICANT: Xu, H. Howard
 TITLE OF INVENTION: Identification of Essential Genes in
 FILE REFERENCE: ELTRA.011A
 CURRENT APPLICATION NUMBER: US/09/815,242
 CURRENT FILING DATE: 2001-03-21
 PRIORITY APPLICATION NUMBER: 60/191,078
 PRIORITY FILING DATE: 2000-03-21
 PRIORITY APPLICATION NUMBER: 60/206,848
 PRIORITY FILING DATE: 2000-05-23
 PRIORITY APPLICATION NUMBER: 60/207,727
 PRIORITY APPLICATION NUMBER: 60/253,625
 PRIORITY FILING DATE: 2000-11-27
 PRIORITY APPLICATION NUMBER: 60/257,931
 PRIORITY FILING DATE: 2000-12-22
 PRIORITY APPLICATION NUMBER: 60/269,308
 PRIORITY FILING DATE: 2001-02-16
 NUMBER OF SEQ ID NOS: 14110
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 11860
 LENGTH: 286
 TYPE: PRT
 ORGANISM: *Pseudomonas aeruginosa*

RESULT 8
 US-09-900-037A-29
 Sequence 29, Application US/09940037A
 Patent No. US20020127679A1
 GENERAL INFORMATION:
 APPLICANT: Kimoto, No. US20020127679A1hiro
 APPLICANT: Yamamoto, Hiroyuki
 APPLICANT: Misuhashi, Kazuya
 TITLE OF INVENTION: NOVEL CARBONYL REDUCTASE, METHOD FOR PRODUCING SAID ENZYME, DNA
 TITLE OF INVENTION: ENCODING SAID ENZYME, AND METHOD FOR PRODUCING ALCOHOL USING SA
 FILE REFERENCE: 06501-050001
 CURRENT APPLICATION NUMBER: US/09/940,037A
 CURRENT FILING DATE: 2000-08-27
 PRIORITY APPLICATION NUMBER: 09/468,738
 PRIORITY FILING DATE: 1999-12-21

us-09-815-242-11860

Query Match 27.2%; score 351; DB 10; Length 286;

Best Local Similarity 35.3%; Pred. No. 2.7e-25; Matches 89; Conservative 49; Mismatches 98; Indels 16; Gaps 6;

QY 4 RLDGKVALITGGTGLGIGLATAKFKVEGAKVMTDRHSVGEKAAK-----SVGTPDQI 57
Db 39 KLEGKALVYTGDSGIGLATAKFKVEGAKVMTDRHSVGEKAAK-----SVGTPDQI 57
QY 58 QFQHDSSEDDGWTKLFDKDATEKAFGVSTLVNAGTAVNKS-VEEMTAENRKLAVNL 116
Db 95 LAFAGDVADAGFCRQVDTLQRKGRLDVLYNAGSQQHQPQRLEDISEEQKETFRNIF 154QY 117 GVEFGTTRGLIORMKNGLGASINNMSIEGVGDPDSLGAVNASKAVRIMSKSAALCAL 176
Db 155 GMFOLTKAALPML--GKGGAINTSITAYKGPNPOLIDYSSTKGAITSFTRSLSMN-L 209QY 177 KDDYDVRVNTHPGVYKTPVLDLPGAEAMSQRTKTPMGHIGEPNDIAYICWYLASENK 236
Db 210 VNRGIRVNAVAPGPIWPLIPSTESAEKVAHFFGADTPMGRGQPEELAASYVYLACNDSS 269QY 237 FATGSEFVWDGG 248
Db 270 YVSGQVLHVNCG 281RESULT 10
US-09-931-186-17; Sequence 17, Application US/09931186
; Patent No. US20020132319A1; GENERAL INFORMATION:
; APPLICANT: ABREO, MELYN A.

; APPLICANT: AGREE, CHARLES S.

; APPLICANT: AUST, ROBERT

; APPLICANT: KISSINGER, CHARLES R.

; APPLICANT: MARGOSIAK, STEVE

; APPLICANT: MENG, JERRY J.

; APPLICANT: PELLEMIER, LAURA A.

; APPLICANT: REJTO, PAUL A.

; APPLICANT: SHOWALTER, RICHARD E.

; APPLICANT: TEMPECKY-RUSSELL, ANNA

; APPLICANT: THOMSON, JIM

; APPLICANT: VANDERPOOL, DARIN

; APPLICANT: VILLAFRANCA, J. ERNEST

; TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
; STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION

; TITLE OF INVENTION: OF INHIBITORS THEREOF

; FILE REFERENCE: 0125-0049

; CURRENT APPLICATION NUMBER: US/09/931,186.

; CURRENT FILING DATE: 2001-08-17

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO: 17

; LENGTH: 259
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-931-186-17Db 123 AVNLKGTPLVQAAQALVSNNGRGSIINISSIVGKVQNGGOTNYAASKAGVIGLTOMAA 182
QY 172 LDCALKDQDVRYNTVHPCYIKTPLVDPDQGAEAMSQRTKTPMGHIGEPNDIAYCVL 230
Db 183 RE--LGRHIGCNSVLPGFIATPMTOKV--QKWDKITEMIPMGHIGDPEDVAVWFL 238Db 231 ASNEKFATGSEFVWDGG 248
Db 239 ASEDSGYITGTSVEVTGG 256RESULT 11
US-09-928-295A-468; Sequence 468, Application US/09978295A
; Patent No. US2002015606A1; GENERAL INFORMATION:
; APPLICANT: Ashehnaei, Avi

; APPLICANT: Bakr, Kevin P.

; APPLICANT: Boststein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Etton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Flivaroff, Ellen

; APPLICANT: Fog, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Geritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gimaldi, J. Christopher

; APPLICANT: Gunney, Austin L.

; APPLICANT: Hillian, Kenneth J.

; APPLICANT: Klijn, Ivar J.

; APPLICANT: Koo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2630PC11

; CURRENT APPLICATION NUMBER: US/09/978,295A

; CURRENT FILING DATE: 2001-10-15

; PRIOR APPLICATION NUMBER: 09/918595

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/064249

; PRIOR FILING DATE: 1997-11-03

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/066364

; PRIOR FILING DATE: 1997-11-21

; PRIOR APPLICATION NUMBER: 60/077450

; PRIOR APPLICATION NUMBER: 60/077632

; PRIOR FILING DATE: 1998-03-11

; PRIOR APPLICATION NUMBER: 60/077641

; PRIOR FILING DATE: 1998-03-11

; PRIOR APPLICATION NUMBER: 60/077649

; PRIOR FILING DATE: 1998-03-11

; PRIOR APPLICATION NUMBER: 60/077791

; PRIOR FILING DATE: 1998-03-12

; PRIOR APPLICATION NUMBER: 60/078004

; PRIOR FILING DATE: 1998-03-13

; PRIOR APPLICATION NUMBER: 60/078886

; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/078936

PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/078910
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/078939
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/079294
 PRIOR FILING DATE: 1998-03-25
 PRIOR APPLICATION NUMBER: 60/079656
 PRIOR FILING DATE: 1998-03-26
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 PRIOR APPLICATION NUMBER: 60/080194
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080327
 PRIOR FILING DATE: 1998-04-01
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 PRIOR APPLICATION NUMBER: 60/084441
 PRIOR FILING DATE: 1998-05-06
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 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084600
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 PRIOR APPLICATION NUMBER: 60/084627
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 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084643
 PRIOR FILING DATE: 1998-05-07
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 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085579
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085580
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085573
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match: 26.4%; Score: 340; DB: 9; Length: 270;
 Best Local Similarity: 37.1%; Pred. No. 2.7e-24;
 Matches: 95; Conservative: 44; Mismatches: 93; Index: 24; Gaps: 10;

RESULT 12

US-09-978-697-468 Application US/09978697

Sequence 468, Application US/09978697

Patent No. US20020169284A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker, Kevin P.

APPLICANT: Borstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Kjavin, Ivar J.

APPLICANT: Kuo, Sophia S.

APPLICANT: Nabier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William T.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2630PIC27

CURRENT APPLICATION NUMBER: US/09/978,697

CURRENT FILING DATE: 2001-10-16

PRIOR APPLICATION NUMBER: 09/918585

PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/064249

PRIOR FILING DATE: 1997-11-03

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066364

PRIOR FILING DATE: 1997-11-21

PRIOR APPLICATION NUMBER: 60/077450

PRIOR FILING DATE: 1998-03-10

PRIOR APPLICATION NUMBER: 60/077632

PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077641

PRIOR FILING DATE: 1998-03-12

PRIOR APPLICATION NUMBER: 60/078004

PRIOR FILING DATE: 1998-03-13

PRIOR APPLICATION NUMBER: 60/078886

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/07936

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/079910

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/079939

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/079294

PRIOR FILING DATE: 1998-03-25

PRIOR APPLICATION NUMBER: 60/079656

PRIOR FILING DATE: 1998-03-26

PRIOR APPLICATION NUMBER: 60/079664

PRIOR FILING DATE: 1998-03-27

PRIOR APPLICATION NUMBER: 60/079689

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PRIOR FILING DATE: 1998-03-27

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PRIOR FILING DATE: 1998-03-27

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PRIOR APPLICATION NUMBER: 60/079920

PRIOR FILING DATE: 1998-03-30

PRIOR APPLICATION NUMBER: 60/079933

PRIOR FILING DATE: 1998-03-30

PRIOR APPLICATION NUMBER: 60/080105

PRIOR FILING DATE: 1998-03-31

PRIOR APPLICATION NUMBER: 60/080107

PRIOR FILING DATE: 1998-03-31

PRIOR APPLICATION NUMBER: 60/080165

PRIOR FILING DATE: 1998-03-31

PRIOR APPLICATION NUMBER: 60/080194

PRIOR FILING DATE: 1998-03-31

PRIOR APPLICATION NUMBER: 60/080327

PRIOR FILING DATE: 1998-04-01

PRIOR APPLICATION NUMBER: 60/080328

PRIOR FILING DATE: 1998-04-01

PRIOR APPLICATION NUMBER: 60/080333

PRIOR FILING DATE: 1998-04-01

PRIOR APPLICATION NUMBER: 60/080334

PRIOR FILING DATE: 1998-04-01

PRIOR APPLICATION NUMBER: 60/080334

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PRIOR FILING DATE: 1998-04-08

PRIOR APPLICATION NUMBER: 60/081071

PRIOR FILING DATE: 1998-04-08

PRIOR APPLICATION NUMBER: 60/081195

PRIOR FILING DATE: 1998-04-08

PRIOR APPLICATION NUMBER: 60/081203

PRIOR FILING DATE: 1998-04-09

PRIOR APPLICATION NUMBER: 60/081229

PRIOR FILING DATE: 1998-04-09

PRIOR APPLICATION NUMBER: 60/081955

PRIOR FILING DATE: 1998-04-15

PRIOR APPLICATION NUMBER: 60/081817

PRIOR FILING DATE: 1998-04-15

PRIOR APPLICATION NUMBER: 60/081819

PRIOR FILING DATE: 1998-04-15

PRIOR APPLICATION NUMBER: 60/081952

PRIOR FILING DATE: 1998-04-15

PRIOR APPLICATION NUMBER: 60/081838

PRIOR FILING DATE: 1998-04-15

PRIOR APPLICATION NUMBER: 60/082568

PRIOR FILING DATE: 1998-04-21

PRIOR APPLICATION NUMBER: 60/082569

PRIOR FILING DATE: 1998-04-21
 PRIOR APPLICATION NUMBER: 60/082704
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/082804
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/082700
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/082797
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/082796
 PRIOR FILING DATE: 1998-04-23
 PRIOR APPLICATION NUMBER: 60/083336
 PRIOR FILING DATE: 1998-04-27
 PRIOR APPLICATION NUMBER: 60/083322
 PRIOR FILING DATE: 1998-04-28
 PRIOR APPLICATION NUMBER: 60/083392
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083495
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083496
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 PRIOR APPLICATION NUMBER: 60/083559
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 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083742
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 PRIOR APPLICATION NUMBER: 60/085700
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 PRIOR APPLICATION NUMBER: 60/085689
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085579
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 PRIOR APPLICATION NUMBER: 60/085580
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 PRIOR APPLICATION NUMBER: 60/085573
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PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697
 Query Match 26.4%; Score 340; DB 9; Length 270;
 Best Local Similarity 37.1%; Pred. No. 2.7e-24; Mismatches 93; Indels 24; Gaps 10;
 Matches 95; Conservative 44; Gaps 10;
 Qy 4 RIDGKVAVITGGFLGIGIAATKFEVEGAKVMTDRHSVGDGKERAASKVGTTPDQIQFFQHD 63
 Db 6 RYAGKVVVVGGRGIGIGIGIVRNFNSGARVAVICDKDSSGRALQEL--pGAV-FILCD 62
 Qy 64 SSSDEGWTKLFDATEKAFGPVSLVNNAG-LAVNKSVEETTAERKLAVNLDGVFFCT 122
 Db 63 VTFQEDDVTKLVTSETTIRGRGRGCVNNAGHHPPQRPEETSQGFRQLELNLGTYLT 122
 Qy 123 RIGIORM-KNKGIGASINMSIEGFVQDPSLIGAYNASKGARVIMSKAALDALKDLY 181
 Db 123 KLAFLPLVLRKSQG--NVIINISLUGATGQQAQVYVATKGATAMTKALALD-ESPGV 177
 Qy 182 RVNTVHPGYIKPLVDDL----PGA---EAMSQRTKTPGHIGENDIAYICVLAS 232
 Db 178 RVCISPGNIWIPPLWEEALALMDPRAFIREMLAQ---PLGRMGOPAEGVAAVFLAS 233
 Qy 233 NESKEATGSEFVFDGG 248
 Db 234 -EANFCTGIELLVLTGG 248

RESULT 13
 US-09-978-192A-468
 Sequence 468, Application US/09978192A
 Patent No. US2002017553A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Olang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillian, Kenneth J.
 APPLICANT: Kiljavin, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: P26301C9
 CURRENT APPLICATION NUMBER: US/09/978, 192A
 CURRENT FILING DATE: 2001-10-15
 PRIOR APPLICATION NUMBER: 09/918585
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/064249
 PRIOR FILING DATE: 1997-11-03
 PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085689
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085579
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085580
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085573
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 26.4%; Score 340; DB 9; Length 270;
 Best Local Similarity 37.1%; Pred. No. 2.7e-24; Mismatches 93; Indels 24; Gaps 10;

QY 4 RLDGKPAITNGTAGLARAKFEEGAKVMTORHSDVGKEAKAKSVGPPDQIQFFQHD 63
 Db 6 RYAGKVVVYFGGRIGAGIVRAFNNSGARVNCICDESGRALEQEL--PGAV-FILCD 62

QY 64 SSDENGWTKLFDATKAFGVSTLVNNAG-TAVNNSVEETTAERKLLAVNLQCFGGT 122
 Db 63 VTOEDDVKVLSETIRREGLDCVVNNAGHHPPQRPEETSAQFRQRLLENLKGTYTL 122

QY 123 RUGIFORM-KKKGIGLSIINNSIECGFVGDPDSLGAYNASKAVRIMSKSALDCALKDYDV 181
 Db 123 KLAUPLRKSQG--NVINNISLVLGAIGOAQAVPVATGAVTMTKALLAD--ESPGV 177

QY 182 RUVWVHPGTTKPLUDL---PGA--EAMNSORTKUPMGHNGERNDIAYCIVYLAS 232
 Db 178 RVCNCISPGNITWPWHEELALMPDPRATREGMLAQ---PLGRMGQPAEVGAANVELAS 233

QY 233 NESVETATGSEBFVVDGC 248
 Db 234 -EANFCTGIELLWVG 248

RESULT 14

US-09-990-832A-468
 Sequence 468 Application US/09999832A
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker, Kevin P.
 APPLICANT: Boiststein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillian, Kenneth J.
 APPLICANT: Kijavin, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William T.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2630PC63

CURRENT APPLICATION NUMBER: US/09/999-832A
 CURRENT FILING DATE: 2001-10-24
 PRIOR APPLICATION NUMBER: 09/918885
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/064249
 PRIOR FILING DATE: 1997-11-03
 PRIOR APPLICATION NUMBER: 60/065311
 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/066364
 PRIOR FILING DATE: 1997-11-21
 PRIOR APPLICATION NUMBER: 60/077450
 PRIOR FILING DATE: 1998-03-10
 PRIOR APPLICATION NUMBER: 60/077632
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077641
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077649
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077991
 PRIOR FILING DATE: 1998-03-12
 PRIOR APPLICATION NUMBER: 60/078004
 PRIOR FILING DATE: 1998-03-13
 PRIOR APPLICATION NUMBER: 60/078886
 PRIOR FILING DATE: 1998-01-20
 PRIOR APPLICATION NUMBER: 60/078936
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/078910
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 PRIOR APPLICATION NUMBER: 60/078939
 PRIOR FILING DATE: 1998-01-20
 PRIOR APPLICATION NUMBER: 60/079294
 PRIOR FILING DATE: 1998-03-25
 PRIOR APPLICATION NUMBER: 60/079556
 PRIOR FILING DATE: 1998-03-26
 PRIOR APPLICATION NUMBER: 60/079664
 PRIOR FILING DATE: 1998-01-27
 PRIOR APPLICATION NUMBER: 60/079689
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079663
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 PRIOR APPLICATION NUMBER: 60/079728
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 PRIOR FILING DATE: 1998-04-08
 PRIOR APPLICATION NUMBER: 60/081195

PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084598
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084600
 PRIOR FILING DATE: 1998-5-07
 PRIOR APPLICATION NUMBER: 60/084627
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084643
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/085339
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085338
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085323
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085582
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085700
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085689
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085579
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085580
 PRIOR FILING DATE: 1998-05-15
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085573
 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match Score 340; DB 9; Length 270;
 Best Local Similarity 26.4%; Score 340; DB 9;
 Matches 95; Conservative 44; Mismatches 93; Indels 24; Gaps 10;

Qy 4 RLDCQKVALITGGTIGLIAKTIKVEEGKVMDTRHSVDGEKAALKSVCVGPPDQIQFQHD 63
 Db 6 RIAGKRVVVVIGGGIGAGIIVRATVNNAG-LAVKSVETTAAWRKLAVNLDSVFFGT 122
 Qy 64 SSBEDGWTKLFDATTEKAGCPVSTLVNNAG-LAVKSVETTAAWRKLAVNLDSVFFGT 122
 Db 63 VTOPODDVKTIVSETTIRRGRLDVCVNNAGHHPVPPORPEETSAQFROLLENLSTVLT 122
 Qy 123 RLQIORM-KNKGASIMSSIGFVGPSLGAKMASKAVRIMSKAADCALKDYV 181
 Db 123 KLAQPYLRSQG--NVINLISSVGAIGQAQAVPVATKGAVTMTKALD--ESPYGV 177
 Qy 182 RVNIVHPGVTKTPVDDL-----PGA--EEAMORTKTPMGHIGEPNDIAYICVYLAS 232
 Db 178 RVNCISPGNIVPWEELALMPPRATREGMIAQ---PLGRMGQPAEVGAAVFLAS 233
 Qy 233 NESKFATSEFVYDGG 248
 Db 234 -EANFCGTGIELLVYDGG 248

Search completed: April 22, 2003, 17:21:49
 Job time : 27 secs

GenCore version 5.1.4-p5-4578
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On protein - protein search, using sw model

Run on: April 22, 2003, 17:14:26 ; Search time 20 seconds

Sequence: US-09-910-033a-2
1 MSNRLDGKVAILRGTLGIG.....NESKFRATGSEFWVNDGGYTAQ 252

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	ALIGMENTS
1	470	36.4	261	2	EB7279 hypothetical protein CCC0246 [Imported] - Caulobacter crescentus	RESULT 1
2	464.5	36.0	260	2	H70758 probable fabG3 protein	EB7279
3	407.5	31.6	255	1	S10707 20beta-hydroxytert	Hypothetical protein
4	400.5	31.0	255	1	S39137 glucose 1-dehydrogenase	probable short-chain dehydrogenase
5	393	30.5	254	2	S48129 3(or 17)beta-hydro	probable short-chain dehydrogenase
6	391	30.3	249	2	S47055 hypothetical protein	probable short-chain dehydrogenase
7	383	29.7	256	2	E77474 2-oxoacid:sh	probable short-chain dehydrogenase
8	380	29.5	247	2	E70740 probable fabG2 protein	probable short-chain dehydrogenase
9	374.5	29.0	248	2	F68868 glucose 1-dehydrogenase	probable short-chain dehydrogenase
10	372.5	28.9	253	2	B93284 probable (imported)	probable (imported)
11	371.5	28.8	261	2	JSD0385 glucose 1-dehydrogenase	probable (imported)
12	370.5	28.7	255	2	A33528 glucose 1-dehydrogenase	probable (imported)
13	368	28.5	253	2	B86737 glucose 1-dehydrogenase	probable (imported)
14	367	28.4	258	2	C70885 probable dehydrogenase	probable dehydrogenase
15	366	28.4	272	2	A99950 hypothetical prote	hypothetical protein
16	365.5	28.3	246	2	H77219 3-oxacycl-(acyl) ca	3-oxacycl-(acyl) ca
17	365.5	28.3	263	2	S01227 glucose 1-dehydrogenase	probable (imported)
18	364.5	28.3	255	2	D70635 hypothetical protein	probable (imported)
19	363.5	28.2	261	1	S00813 glucose 1-dehydrogenase	probable (imported)
20	363	28.1	262	2	S02299 glucose 1-dehydrogenase	probable (imported)
21	359	27.8	254	2	A03182 short chain dehydrogenase	probable short-chain dehydrogenase
22	358.5	27.8	261	2	D66269 glucose 1-dehydrogenase	probable short-chain dehydrogenase
23	357.5	27.7	251	2	A13185 glucose 1-dehydrogenase	probable short-chain dehydrogenase
24	357.5	27.7	258	2	D95284 glucose 1-dehydrogenase	probable short-chain dehydrogenase
25	357.5	27.7	261	2	I40225 probable short-chain dehydrogenase	probable short-chain dehydrogenase
26	357.5	27.7	271	2	AC0157 probable short-chain dehydrogenase	probable short-chain dehydrogenase
27	357	27	296	2	E87260 hypothetical protein	hypothetical protein
28	356.5	27.6	248	2	H98258 3-oxacycl-(acyl) ca	3-oxacycl-(acyl) ca
29	356.5	27.6	248	2	A130255	

Db	120 MSKHALKMLAAGKG-NIINTCSVGGLYAWPDIPAYNASKGGVYIQLTKSMAVDY-A-KHQ	Qy	61 QHDSSDEDGWTKLDATEKAFGPVSTLNNAGIAVNKSVETTAEWKKLAVNLDGFFF
Qy	181 VRVNTVHGYIKTPL---VDDLPGK-BAMSORK-TPMGHTGEPNDIAYICVYLSN	Db	58 RDYDSDEWDTLVMAMAVORRGTUNLVNNAGILLPGMNETGRLEDFSRLKINTESFI
Db	: : : : : : : : : : : : : :	C	117 IRYNCVCGGIIDPPLNEKSFLENNNEGLEEKKAKVYKPLRKGKPEEIAVNLFLASD
Qy	234 ESKPATGSEBFVVDQGYTAQ 252	Qy	121 GTRLGQIQRMKNGKLGASIIINMSIIEGFWDPSLGAYNSKGVRIIMSSAALDCALKYD
Db	237 LSSYMTGSAITADCGYTAQ 255	Db	118 GCQGQIAKME--TGGSIINMASSWVLLIEQVAGYSASKA\SLTRAAALSCKRQSYA
RESULT 5			
Sp	3 or 17 beta-hydroxysteroid dehydrogenase (EC 1.1.1.51) - Comamonas testosteronei (ATCC 1	Qy	181 V-RVNTVHGYIKTPLVD-DLP--GAERSAMSORKTPMGHICBPNDAVYICVYLSN
C;Species	Comamonas testosteronei	Db	176 IRRVNSIHPDGIVTPMMQASLPKGVSKEAVLHDPKLNRAGRAYMPERIAOLVLFASD
A;Parity	ATCC 11996	Qy	177 : : : : : : : : : : : : : :
C;Date	14-JUL-1995 #sequence_revision 01-Dec-1995 #text_change 08-Oct-1999	Db	176 GCQGQIAKME--TGGSIINMASSWVLLIEQVAGYSASKA\SLTRAAALSCKRQSYA
C;Accession	S48129; S51780; S15590; S62216; S6182	Qy	177 : : : : : : : : : : : : : :
R;Abalain, J.H.; di Stefano, S.; Amet, Y.; Ouemener, E.; Abalain-Colloc, M.L.; Flach, H.	J. Steroid Biochem. Mol. Biol. 44: 133-139, 1993	Db	236 KFATGSEFVVD 246
A;Title	Cloning, DNA sequencing and expression of (3-17)beta hydroxysteroid dehydrogenase	Db	236 SVMMSGSELHAD 246
A;Reference number	S48129; MUID:93176721; PMID:8389516	Qy	236 KFATGSEFVVD 246
A;Accession	S48129	A;Cross-references	EMBL:X63379
A;Molecule type	DNA	A;Note	the source is designated as pseudomonas testosteronei
A;Residues	1-13, 'VV', 16-254 <ABM>	R;Abalain, J.H.	submitted to the EMBL Data Library, November 1991
A;Cross-references	EMBL:X63379; NID:9312918; PID:CAA44977.1; PID:9312919	A;Reference number	S47055
A;Note	the source is designated as Pseudomonas testosteronei	A;Accession	S47055
R;Yin, S.J.; Vagelopoulos, N.; Lundquist, G.; Joernvall, H.	EUR. J. Biochem. 197: 359-365, 1991	A;Molecule type	DNA
A;Title	Pseudomonas 3-beta-hydroxysteroid dehydrogenase. Primary structure and relation	A;Residues	1-249 <SWA>
A;Reference number	S15390; MUID:91224127; PMID:2026158	A;Cross-references	EMBL:X78863; NID:95220947; PID:CAA56245.1; PID:9520952
A;Accession	S15390	C;Superfamily	ribitol dehydrogenase; short-chain alcohol dehydrogenase homology <SADH>
A;Molecule type	protein	F;5-181/Domain	short-chain alcohol dehydrogenase homology <SADH>
A;Residues	2-40, 'E', 11-176, 178-240, 'G', 242-254 <YIN>	Query	5 LDGKVAITGIGLGLAIATKVEEGKVKMIDRHSVGEKAKSVCPTPDQIOPFOHDS
A;Note	the source is designated as Pseudomonas testosteronei	Match	65 SDENGWTKLFDATFVGVSTLNNAGAVNSVEETTAENRKLAVNLDCVFFGRL 124
R;Benach, J.; Knapp, S.; Oppermann, U.C.T.; Haegglin, O.; Joernvall, H.; Ladenstein, R.	EUR. J. Biochem. 236, 144-148, 1996	Db	60 TDERAITAMAGKQRALSPITGLVNNAGTAGFSSVHATEVETWSRIMAVNVTGLASKA 119
A;Title	Crystallization and crystal packing of recombinant 3 (or 17) beta-hydroxysteroid	Qy	125 GIORMKNKGIGASTINMSIIEGFGDPSSIGAYNSKGVRIIMSSAALDCALKYDFFF 184
A;Reference number	S62216; MUID:96184891; PMID:8617258	Db	120 ALFGMLERGRGA-TVNFCSVAGLVLGIPMAYCAAKGAVNLTROMADYSGR--GIVRN 176
A;Accession	S62216	Qy	185 TVHGYIK-TPLVDDLFPSAE--BAMSOK-TKPMGHTGEPNDIAYICVYLSNFSRAT 239
A;Status	nucleic acid sequence not shown; not compared with conceptual translation	Db	177 WVCPTGVAGTDMQRQLGTDCDPPEAKRLAKVPMGRGTPEDIAAANVFLSTKAVT 236
A;Molecule type	DNA	Qy	240 GSEFVVDQGYTAQ 251
A;Residues	2-254 <BEN>	Db	237 GSVLAVDQGWTAA 248
A;Cross-references	EMBL:L08971; NID:9309559; PID:AA25742.1; PID:9309860	RESULT 7	
A;Note	the source is designated as Pseudomonas testosteronei	Sp	ET7427
C;Superfamily	ribitol dehydrogenase; short-chain alcohol dehydrogenase homology	C;Keywords	oxidoreductase
C;Keywords	oxidoreductase	C;Species	Thermotoga maritima
F;2-254/Product	3(or 17)beta-hydroxysteroid dehydrogenase homology <SDH>	C;Date	11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
F;8-185/Domain	short-chain alcohol dehydrogenase homology <SDH>	C;Accession	E72427
Query Match	30.5% Score 333 DB 2; Length 254;	R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; H	Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson
Best Local Similarity	36.7% Pred. No. 5, 5e-24;	A;Title	Evidence for lateral gene transfer between Archaea and Bacteria from genome
Matches	92; Conservative 49; Mismatches 100; Indels 10; Gaps 6;	A;Reference number	A72200; MUID:99287316; PMID:10360571
Qy	1 MSNRLDGKVAITGIGLGLAIATKVEEGKVKMIDRHSVGEKAKSVCPTPDQIOPFOHDS	A;Accession	E72427
Db	1 : : : : : : : : : : : : : :	Nature 399, 323-329, 1999	
1 MNRQLGKVALVVGAGSAGVGLVKKLJLGEAKVAFSDINA-AGQOLAAELG--ERSMFV	57		

A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-256 <ARN>
A: Cross-references: GB:AE01690; GB:AE000512; NID:94980496; PIDN:AD35113.1; PID:9498050
A: Experimental source: strain MSB8
C: Genetics:
A: Gene: TM0019
C: Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
Query Match 29.7%; Score 383; DB 2; Length 256;
Best Local Similarity 35.5%; Pred. No. 3; 5e-23;
Matches 93; **Conservative** 48; **Mismatches** 95; **Indels** 26; **Gaps** 7;
Qy 5 LDGKVAILTGTLGGLAIATKVEEGAKVMTDRHSVDPG--EKAKSVGTPDQIQQFQ 61
Db 2 LEGKVAVWGGGGATKOLFAGNMKVIAEDEAGVEREELRERGL--DVTFK 59
Qy 62 HDSSBBDGWTFLDATEKAGPVLSTVNNGIAVNRKSVETTAWRKLLAVNLQCVFFG 121
Db 60 TDVADENSVKMRKVKTEVYGVGDVNLAVMSVSKSIFERPLEEWERVIRVNLQCPYIC 119
Qy 122 TRLGSIORMKNGKLGSASINNSIEGFFVGDSPLGAYNASKAVRIMSKSALDCALKD 181
Db 120 SRYCAEMIRG-GGVVINTASTRAFOSEDEPYASKGGLVALTHSLAV--SLSRYHI 176
Qy 182 RYVNVHPCVIKTPLVDDLGCREAMSQRTK-----PMGHIGEPNDIAYICVYLA 231
Db 177 RVVSPGWET-----SEWKKRSLRKPKDLRPLDIPHEQHPAGRIVGNPLDIAHLCVFLA 229
Qy 232 SNE-SKFGTSEPVVDDGGTAQ 252
Db 230 DDEKAGFETGTNFIVDGGTVK 251

RESULT 8

ET0740

probable fabG2 protein - *Mycobacterium tuberculosis* (strain H37RV)

C:Species: *Mycobacterium tuberculosis*
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: ET0740

R. Cole, S.T.; Broch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Delkin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. *Nature* 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome

A:Reference number: ET0500; MUIID:9825987; PMID:9634230

A:Accession: ET0740

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-248 <KUN>

A:Cross-references: GB:299111; GB:AL009126; NID:92633699; PIDN:CAB13250.1; PID:926337

C:Experimental source: strain 168

C:Genetics:

A:Gene: yko07-182

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology <SDH>

Query Match 29.0%; Score 374.5; DB 2; Length 248;
Best Local Similarity 37.5%; Pred. No. 1.6e-22;
Matches 93; **Conservative** 40; **Mismatches** 106; **Indels** 9; **Gaps** 5;

Qy 4 RLDGKVAILTGTLGGLAIATKVEEGAKVMTDRHSVDPG--EKAKSVGTPDQIQQFQ 63
Db 3 KEGKIALVPGTGGTSGLATAKFKVNEGAVVYITGRQNEKAVNQIG--KNTVQYQD 60

A:Cross-references: GB:Z7555; GB:AL123456; NID:93261608; PIDN:CAA99983.1; PID:91419053

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: fabG2

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology <SDH>

Query Match 29.5%; Score 380; DB 2; Length 247;
Best Local Similarity 36.2%; Pred. No. 5.8e-23; Length 247;
Matches 92; **Conservative** 52; **Mismatches** 94; **Indels** 16; **Gaps** 4;

Qy 1 MSNRDQDGKVAITGGTIGLAIATKVEEGAKVMTDRHSVDPG--EKAKSVGTPDQIQQF 60
Db 1 MASLNKARTAVITGGAGCQGLAIGORVFAEGARVWLDVNLETEVAKRIGGDDVALV 60

Qy 61 QHDSSDDEGWTKFLDATEKAGPVLSTVNNGIAVNRKSVETTAWRKLLAVNLQCVFF 120
Db 61 RCDYTDQDPPDVLLRTAVVERFGGLDWNNAQGKTRDAMRTMTEEDQVIAVHLKGJWN 120

Qy 121 GTRLGIGORMKNGKLGSASINNSIEGFFVGDSPLGAYNASKAVRIMSKSALDCALKD 180
Db 121 GTRLGIGORMKNGKLGSASINNSIEGFFVGDSPLGAYNASKAVRIMSKSALDCALKD 180

Qy 121 GTRLGIGORMKNGKLGSASINNSIEGFFVGDSPLGAYNASKAVRIMSKSALDCALKD 180
Db 121 GTRLGIGORMKNGKLGSASINNSIEGFFVGDSPLGAYNASKAVRIMSKSALDCALKD 180

RESULT 9

ET0740

glucose 1-dehydrogenase homolog ykvo - *Bacillus subtilis*

C:Species: *Bacillus subtilis*
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C:Accession: 69868

R. Kunst, F.; Ogasawa, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berger, C.; Bron, S.; Brunillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, J.; Fleischmann, R.; Goto, T.; Hain, C.; Hauer, J.; Hensel, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.; Ich, J.; Harwood, C.R.; Hennat, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.; Kettler, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino, Y.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete, Y.; Rieger, M.; Rivoira, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Sano, A.; Schleicher, S.; Schroeder, R.; Sofrone, F.; Sekiguchi, J.; Sepowska, A.; Sei, A.; Ueda, M.; Tamakoshi, A.; Tanka, T.; Terpstra, P.; Toononi, A.; Tosato, V.; Uchiya, T.; Winters, P.; Yipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, A.; Authors: Yoshihara, H.F.; Zunstein, E.; Yoshihara, H.; Danchin, A.; Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*
A:Reference number: AD9580; MUIID:9804033; PMID:9380377

A:Accession: F69868

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-248 <KUN>

A:Cross-references: GB:299111; GB:AL009126; NID:92633699; PIDN:CAB13250.1; PID:926337

C:Experimental source: strain 168

C:Genetics:

A:Gene: yko07-182

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology <SDH>

Query Match 29.0%; Score 374.5; DB 2; Length 248;
Best Local Similarity 37.5%; Pred. No. 1.6e-22;
Matches 93; **Conservative** 40; **Mismatches** 106; **Indels** 9; **Gaps** 5;

Qy 4 RLDGKVAILTGTLGGLAIATKVEEGAKVMTDRHSVDPG--EKAKSVGTPDQIQQFQ 63
Db 3 KEGKIALVPGTGGTSGLATAKFKVNEGAVVYITGRQNEKAVNQIG--KNTVQYQD 60

Qy 64 SSDEDGWTKFLDATEKAGPVLSTVNNGIAVNRKSVETTAWRKLLAVNLQCVFFG 123
Db 61 ISKLEDLDKLYDIKOEGKLDILFANAGIGNFLPGCETEQVDRTEFDINKGIFTVQ 120

Qy 124 LGIORMKNGKLGSASINNSIEGFFVGDSPLGAYNASKAVRIMSKSALDCALKD 183
Db 121 KALSLPDK--WGSILVTGSTAGSIGNPAFFSYVGASAALKRVLWILD--LKGTEIRV 176

Qy 184 NTVHPCVIKTPLVDDLGCREAMSQRTK-----PMGHIGEPNDIAYICVYLA 240
Db 177 NVVSPGQILPTAYDELFQDALEEVLEBNSRNTVPAKGVTPEEVANAVSFLASDESYL 236

Qy 241 SEFVVDGG 248

Db 237 VELFVDGG 244

RESULT 10

B92584

probable [imported] - *Sinorhizobium meliloti* (strain 1021) magplasmid pSymA
C:Species: *Sinorhizobium meliloti*
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001

C;Accession: B95284
 R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows-
 ell, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surycki, R.; Wells, D.H.; Yeh, K.C.
 proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
 A;Title: Nucleotide sequence and predicted functions of the entire *sinorhizobium meliloti*
 A;Accession: B95284
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-253 <KUR>
 A;Cross-references: GB:AE005469; PIDN:AAK64826.1; PID:914523249; GSPDB:GN0165
 A;Experimental source: strain 1021, megaplasmid pSma
 R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhier, A.; Abola, P.; Barloy-Hubler, F.;
 Pela, D.; Chain, P.; Covic, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.; Science 293, 668-672, 2001
 A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaire,
 heault, P.; Vandebol, M.; Vorhofer, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
 A;Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
 A;Reference number: A96039; MUID:21368234; PMID:11474104
 A;Contents: annotation
 C;Genetics:
 A;Gene: Sma0329
 A;Genome: plasmid
 C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
 Query Match 28.9%; Score 372.5; DB 2; Length 253;
 Best Local Similarity 37.7%; Pred. No. 2.4e-22;
 Matches 97; Conservative 46; Mismatches 93; Indels 21; Gaps 8;
 Oy 1 MSNRLDGKVAILTGGTGLGIGLAIATKFVEGAKVMTDRH---SDYGEAKNSKGVRPDQ 56
 Db 1 MSNRLDGKVAILTGGTGLGIGLAIATKFVEGAKVMTDRH---SDYGEAKNSKGVRPDQ 56
 Qy 57 IQFFQHSSDEDGWTKLFDATKEAGPVSTLVNNAGIAVANKSVEETTAENRKLAVLD 116
 Db 56 SGIFVANTSSRPPCDAVLAVATVERGRIDTVNAAGMFVTOEEDSDQDADECIASDLS 115
 Qy 117 GVFEGTRIGIORMK-NKGASINMMSRGFVGPSLGAAYNAKGAVRIMSKAALDCA 175
 Db 116 GVFYMSRAVPHLKEIKG---SIVNIGSVSSLGGMSHAAXNARKGGVANLRTSSA-CD 170
 Qy 176 LKDYDVRVNTVHGYIKPLFLDDLGAEEMSORT--KTPGHIGHEDNIAVIVYLASN 233
 Db 171 LGKFGVRANTVAPGLTVTGKVEAIMD-DDALLEKAWDRIPRLRAGQ---ASAVAFLASD 226
 Qy 234 ESKFATGSEFFVWGGYT 250
 Db 227 EAATITGIVLPVPGQQT 243
 RESULT 11
 JS0385 glucose 1-dehydrogenase (EC 1.1.1.47) - *Bacillus megaterium*
 C;Species: *Bacillus megaterium*
 C;Accession: 07-1990 #sequence_revision 07-Sep-1990 #text_change 11-Jun-1999
 C;Fermat, T.; Ebora, R.V.; Nakai, T.; Makino, Y.; Negoro, S.; Urabe, I.; Okada, H.
 A;Title: Structure of isozyme genes of glucose dehydrogenase from *Bacillus megaterium* IAP
 A;Reference number: 139850
 A;Accession: 139852
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-261 <RES>
 A;Cross-references: GB:D90043; NID:91216265; PIDN:BA14099.1; PID:9216268
 A;Experimental source: strain IAM01030
 C;Complex: homotetramer
 C;Function:
 A;Description: catalyzes NAD(P)-dependent dehydrogenation of D-glucose.
 C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
 C;Keywords: oxidoreductase
 F:8-189/Domain: short-chain alcohol dehydrogenase homology <SADH>
 Query Match 28.7%; Score 370.5; DB 2; Length 261;
 Best Local Similarity 33.6%; Pred. No. 3.6e-22;
 Matches 86; Conservative 51; Mismatches 108; Indels 11; Gaps 4;
 Oy 1 MSNRLDGKVAILTGGTGLGIGLAIATKFVEGAKVMTDRH---SDYGEAKNSKGVRPDQ 55
 Db 1 MSNRLDGKVAILTGGTGLGIGLAIATKFVEGAKVMTDRH---SDYGEAKNSKGVRPDQ 55
 Qy 56 QIOPFHSSDEDGWTKLFDATKEAGPVSTLVNNAGIAVANKSVEETTAENRKLAVLD 115
 Db 61 AV---KDVIVESDVINVWOSAKEYPGRKLDVMINNAGLENPVSHMSLDWNKVIDNL 117
 Qy 116 DCVFGTRIGIORMKNGKGLASINMMSIEGVGDPGSLGAAYNAKGAVRIMSKAALDCA 175
 J;Fermat, T.; Ebora, R.V.; Nakai, T.; Makino, Y.; Negoro, S.; Urabe, I.; Okada, H.
 A;Title: Structure of isozyme genes of glucose dehydrogenase from *Bacillus megaterium* IAP
 A;Reference number: 139850
 A;Accession: 139852
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-261 <RES>
 A;Cross-references: GB:D90043; NID:91216265; PIDN:BA14099.1; PID:9216268
 A;Experimental source: strain IAM01030
 C;Complex: homotetramer
 C;Function:
 A;Description: catalyzes NAD(P)-dependent dehydrogenation of D-glucose.
 C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology <SADH>
 C;Keywords: oxidoreductase
 F:8-189/Domain: short-chain alcohol dehydrogenase homology <SADH>
 RESULT 13
 B86737 acetooin dehydrogenase (EC 1.1.1.5) [imported] - *Lactococcus lactis* subsp. *lactis* (s
 Query Match 28.8%; Score 371.5; DB 2; Length 261;
 Best Local Similarity 34.2%; Pred. No. 3e-22;
 Matches 88; Conservative 51; Mismatches 105; Indels 13; Gaps 5;
 Db 1 MYKDLGKVKVWITGSGTIGKAMIAFTEAKVWVNTFSKE-EEANSYLEELKKVG-- 56
 Qy 55 DQ1OFFHSSDEDGWTKLFDATKEAGPVSTLVNNAGIAVANKSVEETTAENRKLAVN 114
 Db 57 GEAIAVKGDTVYESDVINVQVSSIKEFGKLDVMINNAGENPVSSHEMSLDWNKVIDN 116
 Qy 115 LDGVFGCTRLGIGLAKTKEGVVNGKASIIINMSIEGVGDPGSLGAAYNAKGAVRIMSKAALDC 174
 Db 117 LTGAFGLSREAJYFVENDIKGIVNMSVHEKIPWPLFVHYAASKGKLMTALLEY 176
 Qy 175 ALKDYDVRVNTVHGYIKPL-VDLPGAEAMSQRTKPMGHIGEPNIMIAYCIVLASN 233
 Db 177 APK--GIRVNNITPGGAINTPINAKFAEKFADPFPQRADVESMIPMGYIGEPEELAAVAWLASS 234
 Qy 234 ESKFATGSEFFVWGGYT 250
 Db 235 EASYVIGITLFDAGGTT 251

N;Alternate names: acetyl reductase
 C;Species: Lactococcus lactis subsp. lactis
 C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
 C;Accession: B86737
 R;Bolotin, A.; Windker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlich, S.; Genome Res. 11, 731-753, 2001
 A;Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* ss
 A;Reference number: A86625; MUID:21235186; PMID:11337471
 A;Accession: B86737
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-253 <STO>
 A;Cross-references: GB:AE005176; PID:912723829; PIDN:AAK04996.1; GSPDB:GN00146
 A;Experimental source: strain IL1403
 C;Genetics:
 A;Gene: butA
 C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
 C;Keywords: oxidoreductase

Query Match 28.5%; Score 368; DB 2; Length 253;
 Best Local Similarity 34.3%; Pred. No. 5.4e-22; Mismatches 103; Indels 14; Gaps 4;
 Matches 86; Conservative 48; Mismatches 103; Indels 14; Gaps 4;

QY 8 KVALITGGIGLAIATKVERGAKVMTDRSDVGKAASVGTPOIQFOHDSDE 67
 Db 3 KIAAVTGACGIGFAIARKLYNDGFKVAKIDNEETAAKAKELG - ENSFAK1ADYSDR 60

QY 68 DGTWTKLFATEKAFGPVSTLVLNNAGIAVNNKSYETTAERWLKLLAVNLGDFVFGTRLGQ 127
 Db 61 EQVITALNAAVDRGFLKVVNNAGIAPTOQIPTPEOFHQVNTINVGGVWGTQSTA 120
 128 RMRNKIGIGASINMSIEFGVGDPSLGYNAASKGAVRIMSKSALDCAKDYDVRVNVH 187
 Db 121 LFRKLGHGKINATNSQAGVSNPMLYSSKFAVRGNTQTAARD - LAEGCITVNRAYA 178

QY 188 PSYKTFPLDLE-----PGAEAMSOPT--KTPMCHIGERENDIAVICVLASNSKE 237
 Db 179 PGIVKTPMFDIAHOGVKNAGKDEQMQTFAKDIAKRLSPEDVANVVSFLAGPSNY 238

QY 238 ATGSEFVVDGG 248
 Db 239 ITQQTIVDGG 249

RESULT 14

C70885 probable dehydrogenase - *Mycobacterium tuberculosis* (strain H37RV)
 C;Species: *Mycobacterium tuberculosis*
 C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
 C;Accession: C70885
 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998
 A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A;Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
 A;Reference number: A70500; MUID:98295987; PMID:9634230
 A;Accession: C70885
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-258 <COL>
 A;Cross-references: GB:AL008883; GB:AL123456; NID:93261490; PIDN:CRA15519.1; PID:9261280
 A;Experimental source: strain H37Rv
 C;Genetics:
 A;Gene: RV2857c
 C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
 F;11-88/Domain: short-chain alcohol dehydrogenase homology <SDH2>

Query Match 28.4%; Score 367; DB 2; Length 258;
 Best Local Similarity 35.7%; Pred. No. 6.7e-22;
 Matches 92; Conservative 45; Mismatches 105; Indels 16; Gaps 7;

Db 4 LSQRLLAGRIVAVIIGGGSGIGLAGRMRRAEGATIVVGDVDEAGAA----DELSGL 57
 QY 59 FQFDSSSDGWTLFDATEKAGCPVSTLVNNAGIA - VNKSVETTAERWLKLLAVNL 116
 Db 58 FVPTDVCDDEAVNLFDGAAETYGRIDIAFNNAGISPPEDNLTTELAAWORVODNLK 117
 QY 117 GVFCTRLGIQRMNKLGASINNSIEFGVGD-PSLGAIVNASKGAVRIMSKSALDCA 175
 Db 118 SVLCCRAALRHYMLAGK-SVNTASEPVAWGSATSDISYTSKGGVLAMSLRGQFA 176
 QY 176 LKDYDVWVWVHRYIKPLVDDI--PGAEAMSQRTKTPMWHIGEPNDIAVTCVYLAS 233
 Db 177 RQ-GIRVNAALCPGPNTPLQLEFLAKNPERARRMWHVPLGRFAEPDEIAVAVAFASD 234
 QY 234 ESKFATGSEFVVDGGYTA 251
 Db 235 DASPISTASFLVBDGGSS 252

RESULT 15

A99550 hypothetical protein SA2260 [imported] - *Staphylococcus aureus* (strain N315)
 C;Species: *Staphylococcus aureus*
 C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 C;Accession: A99550
 R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oma, A.; Mizutani-Ui, Y.; Ogawa, N.; Swano, T.; Inoue, R.; Kaijo, C.; Sekimizu, K.; Lancet 357, 1225-1240, 2001
 A;Title: Whole genome sequencing of meticillin-resistant *Staphylococcus aureus*.
 A;Reference number: A89758; MUID:21311952; PMID:11418146
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-272 <KUR>
 A;Cross-references: GB:BA000018; PID:913702422; PIDN:BA843563.1; GSPDB:GN00146
 A;Experimental source: strain N315
 C;Genetics:
 A;Gene: SA2260
 C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 28.4%; Score 366; DB 2; Length 272;
 Best Local Similarity 35.4%; Pred. No. 8.6e-22; Mismatches 108; Indels 14; Gaps 6;
 Matches 91; Conservative 44; Mismatches 108; Indels 14; Gaps 6;

QY 4 RDGKVAVITGGIGLIGLAIATKVERGAKVMTDRSDVGKAASVGTPOIQFOHD 63
 Db 3 RLENKVAVVTGAGTGIGOSAVALAOGEGAYLAVDIEAVSTVDKTSNSDNKAVND 62

QY 64 SDEDGWTKLFATEKAFGPVSTLVLNNAGI - AVNNKSYETTAERWLKLLAVNLGFF 121
 Db 63 1SDEQQVWDFVSDIKRGPDRGIVDLEFLNNAGVNAAGR-IHEPFDVDKIMMDRSTIL 121
 QY 122 TRLGQRMNKLGASINNSIEFGVGDPSLGYNAASKGAVRIMSKSALDCAKDYV 181
 Db 122 TKNMLPLAMMNO--GGSIVNTSSFGSGAEDLYRSGYNAAKGAVINFKSIAIEG-RD-GI 177
 QY 182 RYNTVHRYIKPLVLDLPGABE-----AMQRKTPMCHIGERNDIATCVYLASNE 234
 Db 178 RNSNAAPIGTIEPPLVDKLTGTSEDDACKTFRENOKWMTPLGRGKPEEVAKLUVFLASD 237
 QY 235 SRFATSEFVVDGGYTA 251
 Db 238 SSFITGEPTRIDGGVA 254

Search completed: April 22, 2003, 17:16:52

Job time : 22 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Title: US-09-910-033a-2

Perfect score: 1290

Sequence: 1 MSNRIDGKVALITGGTIGIG.....NESKFATGSEFVVDGGYTAQ 252

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database : Swissprot_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	464.5	36.0	260	1	YK02_MYCTU	YK02_MYCTU STANDARD; PRT: 260 AA.
2	441.5	34.2	250	1	LINK_PSEPA	Q10855 mycobacteri
3	407.5	31.6	255	1	2BHD_STREX	P50198 pseudomonas
4	400.5	31.0	255	1	YKFD_BACSU	P19992 streptomyce
5	383	29.7	256	1	YQ19_THEME	P39640 bacillus su
6	380	29.5	247	1	YD50_MYCTU	056318 thermotoga
7	371.5	28.8	261	1	DHG1_BACME	Q11020 mycobacteri
8	370	28.7	261	1	DHG4_BACME	P39482 bacillus me
9	370	28.7	253	1	3BHD_COMTE	P40288 bacillus me
10	365.5	28.3	246	1	DHG4_THEME	P19871 comamonas t
11	363.5	28.2	261	1	DHG4_BACME	Q9x248 thermotoga
12	360	27.9	262	1	DHG4_BACME	P10528 bacillus me
13	358.5	27.8	261	1	DHG_BACSU	P07999 bacillus me
14	357.5	27.7	261	1	DHG4_BACME	P12310 bacillus su
15	355.5	27.6	261	1	DHG2_BACME	P39483 bacillus me
16	352.5	27.3	261	1	DHG3_BACME	P39484 bacillus me
17	352.5	27.2	251	1	Y325_THEME	09wy90 thermotoga
18	348.5	27.0	258	1	DHG2_BACSU	P0806 bacillus su
19	345	26.7	261	1	DHB8_HUMAN	Q92506 homo sapien
20	339.5	26.3	256	1	BUDC_KLEPN	Q84436 klebsiella
21	326	25.3	285	1	GS39_BACSU	P80873 bacillus su
22	325.5	25.2	260	1	DHB8_MOUSE	P50171 mus musculus
23	324	25.1	336	1	TS21_MAZE	P50160 zea mays (m
24	322	25.0	289	1	YHDF_BACSU	007575 bacillus su
25	321	24.9	248	1	FABG_CHLMO	Q9PK77 chlamydia m
26	321	24.9	548	1	YAVI_RHISN	Q53217 rhizobium s
27	319.5	24.8	256	1	GNO_GIJOX	P50199 gluconobact
28	319.5	24.8	258	1	BDRA_RHIME	086034 rhizobium m
29	318	24.7	244	1	FABG_VIBCH	Q9Kq97 vibrio chol
30	317.5	24.6	262	1	VER1_APPA	P50161 aspergillus
31	317	24.6	241	1	PHBB_ZOORA	P23238 zoogloea ra
32	316	24.5	246	1	FABG_BACSU	P51831 bacillus su
33	316	24.5	281	1	SOUL_CANAL	P87219 candida alb

ALIGNMENTS

34	313.5	24.3	264	1	STCU_EFMENT	000791 emericella
35	312	24.2	241	1	PHBB_RHIME	P50205 rhizobium m
36	312	24.2	248	1	FABG_AQUAC	067610 aquifex aeo
37	310.5	24.1	271	1	SDRL_PICAB	P08632 picab abeo
38	310	24.0	273	1	TRNL_DATST	P50162 datura stra
39	307.5	23.8	250	1	LINC_PSEPA	P50197 pseudomonas
40	305	23.6	247	1	FABG_CHLTR	P38004 bacillus su
41	305	23.6	285	1	YHXC_BACSU	P40397 bacillus su
42	304.5	23.6	248	1	FABG_CHLPN	Q928P2 chlamydia p
43	303	23.5	278	1	Y4LA_RHISN	P55541 rhizobium s
44	301.5	23.4	320	1	FABG_CUPLA	P28643 cuphea lanc
45	299.5	23.2	253	1	Y4MP_RHISN	P55575 rhizobium s

DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00051; ADH_SHORT; 1.
 DR HYPOTHETICAL PROTEIN; OXIDOREDUCTASE; NAD; COMPLETE PROTEOME.
 FT NP_BIND 11 35 NAD (BY SIMILARITY).
 FT ACT_SITE 153 153 BY SIMILARITY.
 FT ACT_SITE 174 174 S -> G (IN REF. 2).
 FT CONFLICT 9 34 NAD (BY SIMILARITY).
 SQ SEQUENCE 260 AA; 27030 MW; 0935A14ED36220B7 CRC64;
 Best Local Similarity 36.0%; Score 464.5; DB 1; Length 260;
 Matches 106; Conservative 44; Mismatches 90; Indels 11; Gaps 5;
 QY 1 M\$NRUDGKVAITGGTLGIGLAIATKFVERGAKW\$NIDRHSV\$EAKA\$VGTPD\$OIFF 60
 Db 1 M\$GR\$LIGKV\$ALV\$GARG\$GASH\$V\$AMV\$EAK\$V\$FGD\$L\$DEE\$K\$AV\$A\$LA\$- D\$A\$R\$T\$V 58
 QY 61 QHD\$S\$D\$E\$G\$W\$K\$F\$K\$T\$E\$R\$A\$K\$P\$Y\$S\$T\$V\$N\$N\$A\$G\$A\$N\$K\$S\$T\$E\$T\$T\$A\$E\$W\$K\$U\$L\$A\$N\$D\$G\$V\$F\$ 120
 Db 59 HLD\$V\$T\$Q\$P\$Q\$T\$A\$A\$T\$A\$V\$T\$A\$F\$G\$G\$H\$V\$V\$N\$N\$A\$G\$A\$N\$K\$S\$T\$E\$T\$T\$A\$E\$W\$K\$U\$L\$A\$N\$D\$G\$V\$F\$ 118
 QY 121 GTR\$G\$T\$Q\$R\$M\$K\$G\$G\$A\$N\$S\$T\$E\$G\$F\$V\$D\$P\$S\$G\$A\$Y\$N\$A\$S\$K\$G\$A\$V\$W\$K\$M\$K\$S\$A\$A\$D\$C\$A\$K\$D\$Y\$ 180
 Db 119 G\$R\$A\$V\$K\$V\$P\$K\$E\$A\$G\$R\$G\$-S\$N\$I\$S\$S\$E\$G\$L\$A\$G\$T\$V\$A\$C\$H\$Y\$T\$A\$K\$F\$A\$V\$R\$G\$T\$K\$S\$T\$A\$E\$- L\$G\$P\$G\$ 175
 181 V\$R\$V\$V\$W\$H\$P\$Y\$K\$T\$P\$V\$D\$P\$G\$A\$E\$B\$A\$M\$S\$Q\$R\$T\$K\$P\$M\$G\$H\$G\$E\$P\$N\$D\$T\$A\$Y\$I\$C\$V\$L\$A\$N\$S\$K\$F\$A\$T\$G 240
 QY 176 I\$R\$V\$N\$S\$T\$H\$P\$K\$V\$K\$T\$P\$M\$D\$W\$P\$- E\$D\$F\$- -Q\$T\$A\$G\$R\$A\$E\$P\$V\$E\$V\$S\$N\$V\$V\$Y\$L\$A\$D\$B\$S\$Y\$S\$G 229
 QY 241 S\$E\$F\$V\$D\$G\$G\$T\$V\$A\$ 251
 Db 230 A\$E\$F\$V\$D\$G\$G\$T\$V\$A\$ 240

RESULT 2

LINK_PSEPA

ID LINK_PSEPA STANDARD: PRT: 250 AA.
 AC P50198;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DE 2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase (EC 1.1.1.1)
 DE (2,5-DDOL dehydrogenase).
 GN LINX.
 OS Pseudomonas paucimobilis (Sphingomonas paucimobilis).
 OC Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae;
 OC Sphingomonas.
 OC NCBI_TAXID=13689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ST26;
 RX MEDLINE=94253977; PubMed=7515041;
 RA Nagata Y., Ohnmo R., Miyazaki K., Fukuda M., Yano K., Takagi M.;
 RT 'Cloning and sequencing of a 2,5-dichloro-2,5-cyclohexadiene-1,4-diol
 RT dehydrogenase gene involved in the degradation of gamma-
 RT hexachlorocyclohexane in Pseudomonas paucimobilis.';
 RL J. Bacteriol. 176:3117-3119 (1994).
 CC -I- FUNCTION: DEGRADATION OF 2,5-DICHLORO-2,5-CYCLOHEXADIENE-1,4-DIOL
 CC (2,5-DDOL) INTO 2,5-DICHLOROHYDROQUINONE (2,5-DHQ). LINX IS NOT
 CC ESSENTIAL TO GAMMA-HCH DEGRADATION.
 CC -I- PATHWAY: DEGRADATION OF GAMMA-HEXACHLOROCYCLOHEXANE.
 CC -I- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC

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RESULT 3

BHD_STREX

ID BHD_STREX STANDARD: PRT: 255 AA.
 AC P19992;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE 20-beta-hydroxy steroid dehydrogenase (EC 1.1.1.53).
 OS Streptomyces exfoliatus (Streptomyces hydrogenans).
 OC Bacteria; Actinobacteria; Actinomycetidae; Actinomycetales; Streptomyces;
 OC Actinomycetales; Streptomyces; Streptomyctaceae; Streptomyces.
 OC NCBI_TAXID=1905;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=90306362; PubMed=2194840;
 RA Marekov L., Krook M., Joernvall H.;
 RT 'Prokaryotic 20 beta-hydroxysteroid dehydrogenase is an enzyme of the
 RT short-chain, non-metalloenzyme, alcohol dehydrogenase type.';
 RL FEBS Lett. 266:51-54 (1990).
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
 RX MEDLINE=9205221; PubMed=1946424;
 RA Ghosh D., Weeks C.M., Grochulski P., Duax W.L., Erman M.,
 RA Rimsay R.L., Orr J.C.;
 RT 'Three-dimensional structure of holo 3 alpha,20 beta-hydroxysteroid
 RT dehydrogenase: member of a short-chain dehydrogenase family.';
 RL Proc. Natl. Acad. Sci. U.S.A. 88:11060-11068 (1991).
 CC -I- CATALYTIC ACTIVITY: Androstan-3-alpha,17-beta-diol + NAD(+) = 17-
 CC beta-hydroxyandrostan-3-one + NADH.
 CC -I- SUBUNIT: HOMOMEROTRIMER.
 CC -I- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 DR PIR; S10707; S10707.
 DR PDB; 2HS2; 31-AUG-94.
 DR PDB; 1HDC; 07-FEB-95.
 DR InterPro; IPR002198.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.

DE Putative oxidoreductase .TM0019 (EC 1. . . .).
 GN TM0019.
 OS Thermotoga maritima.
 OC Bacteria; Thermotogae; Thermotogales;
 OC Thermomicrobaceae; Thermotoga.
 OC NCBI_TAXID=2336;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MSBB / DSM 3109;
 RX MEDLINE=96125254; PubMed=8550425;
 RA Kletzin A.; Adams M.;
 RT *Molecular and phylogenetic characterization of pyruvate and 2'-
 ketoisovalerate ferredoxin oxidoreductases from *Pyrococcus furiosus*
 and pyruvate ferredoxin oxidoreductase from *Thermotoga maritima*.;
 RL J. Bacteriol. 178:248-257(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MSBB / DSM 3109;
 RX MEDLINE=99387316; PubMed=10360571;
 RA Nelson K.E.; Clayton R.A.; Gill S.R.; Gwynn M.L.; Dodson R.J.;
 RA Haft D.H.; Hickey E.K.; Peterson J.D.; Nelson W.C.; Ketchum K.A.;
 RA McDonald L.; Utterback T.R.; Malek J.A.; Linher K.D.; Garrett M.M.;
 RA Stewart A.M.; Cotton M.D.; Pratt M.S.; Phillips C.A.; Richardson D.;
 RA Heidelberg J.; Sutton G.G.; Fleischmann R.D.; Eisen J.A.; White O.;
 RA Salzberg S.L.; Smith H.O.; Venter J.C.; Fraser C.M.;
 RT *Evidence for lateral gene transfer between Archaea and Bacteria from
 RL a genomic sequence of *Thermotoga maritima*.;
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 (SDR) FAMILY.
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 DR TIGR: TM0019; -
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINS: PR00080; SDRFAMILY.
 DR PROSITE: PS0061; ADH_SHORT; 1.
 DR EMBL: X85171; CAA595959; 1; -
 DR EMBL: AE001690; AAD35113; 1; -
 DR HSSP: 070351; 1E6W.
 DR TIGR: TM0019; -
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINS: PR00080; SDRFAMILY.
 DR PROSITE: PS0061; ADH_SHORT; 1.
 DR KW Hypothetical protein; oxidoreductase; NADP; complete proteome.
 FT NP_BIND 9 33 NADP (BY SIMILARITY).
 FT ACT_SITE 153 153 BY SIMILARITY.
 FT CONFLICT 130 136 RGGVIT -> TRWRSDH (IN REF. 1).
 SQ SEQUENCE 256 AA; 28078 MW: D68160B1D7980C6B CRC64;
 Query Match 29 7%; Score 383; DB 1; Length 256;
 Best Local Similarity 35.5%; Pred. No. 2.9e-24;
 Matches 93; Conservative 48; Mismatches 95; Indels 26; Gaps 7;
 Qy 5 LDGKVAILITGGTGLIGLATAKVEEGAKVMTIDRRSDVG--EKAAGKSVGTPDQIOFQ 61
 Db 2 LECKVWVGGGGCGGAQAALEAENGKWKVIAEDEAVEREEMRLBERGL--DVTFLK 59
 Qy 62 HDSSDEDGWTKLDATEKAFGPVSTLVNNAGTAVNKSVEETTAERWKLUAVLVDGVFG 121
 Db 60 TDVADENSKVNMVRKTVIYGGDVLVNNAAVWSVSKSFERPLEEWRVIRVNLTGPV 119
 Qy 122 TRIGIORMKNGKGAGASLINSSTEGFVCDPSIGAIVNSKGAIRIMSKSALDQKIDV 181
 Db 120 SRYCAEEMIKRG-GGVVINITAATRAFOSEPDPYPSASKGGVVALTHSLAV - SLSRYHI 176
 Qy 182 RYVTHVPSVYKTPPLVDDLPGAAEAMASQRTK-----PMSGICBPNPDIAVYCVLA 231
 Db 177 RYVSIKPWET-----SERKKKSLRKPKDPLRPIHQPGRGVNPLDIAHCVPLA 229

Qy 232 SNB-SKFATGSEFVWDGCGYTAQ 252
 Db 230 DDEKAGFTTGTFNFIVDGOMTVK 251.

RESULT 6
 YD50_MVCTU ID YD50_MVCTU STANDARD; PRM; 247 AA.
 AC 011020; DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE putative oxidoreductase RV1350 (EC 1. . . .).
 GN FABG2 OR RV1350 OR MTI393 OR MTCY02B10.14.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OC NCBI_TAXID=1773;
 RN YD50_MVCTU ID YD50_MVCTU STANDARD; PRM; 247 AA.
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RX MEDLINE=9825987; PubMed=9634230;
 RA Cole S.T.; Brosch R.; Parhille T.; Garnier T.; Churcher C.; Harris D.;
 RA Gordon S.V.; Eiglemeier K.; Gas S.; Barry C.E. III; Tekala F.;
 RA Badcock K.; Basham D.; Brown D.; Chillingworth T.; Connor R.;
 RA Davies R.; Devlin B.; Fellows T.; Gentles S.; Hamlin N.; Holroyd S.;
 RA Hornsby T.; Jagels K.; Krogh A.; McLean J.; Moule S.; Murphy L.;
 RA Oliver S.; Osborne J.; Quail M.A.; Rajandream M.A.; Rogers J.;
 RA Rutter S.; Seeger K.; Skeat S.; Squares S.; Squares R.;
 RA Sulston J.E.; Taylor K.; Whitehead S.; Barrell B.G.;
 RA *Deciphering the biology of *Mycobacterium tuberculosis* from the
 RT complete genome sequence.;
 RL Nature 393:537-544(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oskosh;
 RA Fleischmann R.D.; Alland D.; Eisen J.A.; Carpenter L.; White O.;
 RA Peterson J.; DeBoy R.; Dodson R.; Gwynn M.L.; Haft D.; Hickey E.;
 RA Kolonay J.F.; Nelson W.C.; Umayam L.A.; Ermolayeva M.D.; Salzberg S.L.;
 RA Delcher A.; Utterback T.; Weidman J.; Khouri H.; Gill J.; Mikula A.;
 RA Bishai W.;
 RT *Whole genome comparison of *Mycobacterium tuberculosis* clinical and
 RL laboratory strains.;
 CC Submitted (APR 2001) to the EMBL/GenBank/DDBJ databases
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
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 DR TIGR: MTI393; -
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINS: PR00080; SDRFAMILY.
 DR PROSITE: PS0061; ADH_SHORT; 1.
 DR KW Hypothetical protein; oxidoreductase; NAD; complete proteome.
 FT NP_BIND 9 34 NAD (BY SIMILARITY).
 FT ACT_SITE 155 155 BY SIMILARITY.
 SQ SEQUENCE 247 AA; 25871 MW: 76CA07892E7BBA73 CRC64;
 Query Match 29 5%; Score 380; DB 1; Length 247;
 Best Local Similarity 36.2%; Pred. No. 4.8e-24;
 Matches 92; Conservative 52; Mismatches 94; Indels 16; Gaps 4;

STRAIN=MSB8 / DSM 3109;
 RX MEDLINE=9928316; PubMed=10360571;
 RA Nelson K.E., Clynon R.A., Gill S.R., Gwynn M.L., Dodson R.J.,
 Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
 McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
 Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
 RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.,
 "Evidence for lateral gene transfer between Archaea and Bacteria from
 genome sequence of *thermotoga maritima*,"
 RIL *Nature* 399:323-328 (1999);
 CC -!- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
 CC NAD(P)+ - 3-oxoacyl-[acyl-carrier protein] + NADPH.
 CC -!- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
 CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC
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 CC
 EMBL: AEG001811; Adh36790.1; -
 HSSP: P50162; LAEL.
 DR TIGR; TM174; -
 DR InterPro; IPR002198; ADH_short.
 DR Pfam; PF00105; adh_short; 1.
 DR PRIMIS; PR00061; SDRFAMILY.
 DR PROSITE; PS00061; ADH_SHORT; 1.
 DR FATTY_ACID_BIOSYNTHESIS; OXIDOREDUCTASE; NADP; Complete proteome.
 FT NP_BIND 10 34 BY SIMILARITY.
 FT ACT_SITE 154 264 AA; 26401 MW; 8C08904D280939142 CRC64;
 SQ SEQUENCE 246 AA;
 Query Match 28.3%; Score 365.5; DB 1; Length 246;
 Best Local Similarity 35.1%; Pred No. 7.3e-23;
 Matches 87; Conservative 52; Mismatches 100; Indels 9; Gaps 5;
 OY 4 RLDQKVAVITGTGIGLIGIAINTKFVEEGAKVYKMITDRHSVGEKAASKV-GTPQDQIQFFQH 62
 Db 2 RLEGKVCLITGGAAKGAKITLFAQEGATVIAKGDISKENLDSVKEAEGLPKVDPYL 61
 OY 63 DSSDEDGWVFLDATEKAEGPVSTLVNNAGIAVNSKVEETTAERWLKLAVNLGVFFGT 122
 Db 62 NVTFRDQIKEVVKVVKVQYGRIVDLYVNAGITRBDALLYMKEDDAVINVNLKGVFNT 121
 OY 123 RLGTOORMKNGLGASINNMSIEFGVGDPSLGLAYNASKGAVRIMSKSAALDCALKDYDR 182
 Db 122 QMVVPMYKQRG-SIVVWSSVWGIYGNPGQTNVYASKAVGIVTKWAKELAGR-NTR 178
 OY 183 VNTVHPGVIKTPVLDLPL-GAERAMSGRTKTPGHIGIGPNDAYICVYLASNEKFAAG 240
 Db 179 VNAVAPGVIETPMTEKLPEKARETALS--RIPLGFRGKPEVAQVILFLASDESSYVG 235
 OY 241 SEFVYDGG 248
 Db 236 QVIGIDGG 243

 RESULT 11
 DHGB_BACME STANDARD PRT: 261 AA.
 AC P10528;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Glucose 1-dehydrogenase A (EC 1.1.1.47).
 GN Bacillus megaterium.
 OS Bacillus megaterium.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.
 OX NCBI_TAXID=1404;
 RA [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MI286;
 RX MEDLINE=80271315; PubMed=3134196;
 RA Heilmann H.J., Maeert H.J., Gassen H.G.;
 "Identification and isolation of glucose dehydrogenase genes of
Bacillus megaterium MI286 and their expression in *Escherichia coli*."
 RIL *J. Biotechnol.* 174:485-490 (1998);
 CC -!- CATALYTIC ACTIVITY: Beta-D-glucose + NAD(P)(+)- D-glucono-1,5-
 lactone + NAD(P)H.
 CC -!- SUBUNIT: HOMOTETRAMER.
 CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC
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 CC
 DR EMBL: X12370; CAA30931.1; -
 DR PIR: S00812; S00812.
 DR HSP; P50162; LAEL.
 DR InterPro; IPR002198; ADH_short.
 DR Pfam; PF00106; adh_short; 1.
 DR PRIMIS; PR00061; SDRFAMILY.
 DR PROSITE; PS00061; ADH_SHORT; 1.
 DR KW Oxidoreductase; NADP; Multigene family.
 FT NP_BIND 11 35 BY SIMILARITY.
 FT ACT_SITE 158 158 BY SIMILARITY.
 SQ SEQUENCE 261 AA; 28187 MW; 6FADD3968DC417C CRC64;
 Query Match 28.2%; Score 363.5; DB 1; Length 261;
 Best Local Similarity 31.5%; Pred No. 1.1e-22;
 Matches 82; Conservative 51; Mismatches 108; Indels 19; Gaps 4;
 OY 1 MSNRUDGKVAVITGTGIGLIGIAINTKFVEEGAKVYKMITDRHSVGEKAASKV 51
 Db 1 MYTDIKKVVITGGSTGGRAMAVRFGSEAKVVINYNNEEALDKKEVEEAGGKI 60
 OY 52 GTPDQIOFFQHDSSEDGWVFLDATEKAEGPVSTLVNNAGIAVNSKVEETTAERWLKL 111
 Db 61 -----IVQGDVTRKEEDVNVLVTAIKEFGTLDVMINNAGVNPVSHLSLDWNWKVI 113
 OY 112 AVNLDGVFFCTRLGQIORMKNGLGASINNMSIEFGVGDPSLGLAYNASKGAVRIMSKSA 171
 Db 114 DTNHLGFAFLGSREALKYEVENDIKGNVNTMSSHEMIPMLFYAAASKGGMKMTEFLA 173
 OY 172 LDCALKDYDRVNTVHPGVIKTPVLDLPL-GAERAMSGRTKTPGHIGIGPNDAYICVYL 230
 Db 174 LEYAPK-GIRVNNGP GAMNTPNAERFADPEORADWESWMPGKISKEEVAAVAFL 231
 OY 231 ASNESKFATGSEFVYDGGT 250
 Db 232 ASSOSVYVITLFADGSGMT 251

 RESULT 12
 DHGB_BACME STANDARD PRT: 262 AA.
 AC P07959;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Glucose 1-dehydrogenase B (EC 1.1.1.47).
 GN GDB.
 OS Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.
 OS NCBI_TAXID=1404;

RT	"The complete genome sequence of the Gram-positive bacterium <i>Bacillus subtilis</i> ".	RC	STRAIN=IAM 1030;
RL	Nature 390:249-256(1997).	RX	MEDLINE=92332436; PubMed=1629157;
CC	-i - CATALYTIC ACTIVITY: Beta-D-glucose + NAD(P)(+)-> D-glucono-1,5-lactone + NAD(P)H.	RA	Nakao T.; Mitamura T.; Wang X.H.; Negoro S.; Yomo T.; Urabe I.
CC	-i - SUBUNIT: HOMOTRIMER.	RA	Okada H.
CC	-i - INDUCTION: IT IS INDUCED AT STAGE III OF THE SPORULATION.	RT	"Cloning, nucleotide sequences, and enzymatic properties of glucose dehydrogenase isozymes from <i>Bacillus megaterium</i> IAM1030."
CC	-i - SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.	RL	J. Bacteriol. 174:5013-5020(1992).
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CC	EMBL: M12276; AAA24463.1; -.	CC	-i - SUBUNIT: HOMOTRIMER.
CC	EMBL: D5053; BAA0924.1; -.	CC	-i - MISCELLANEOUS: PREFERENCES NAD TO NADP; 2M NACL ENHANCES ITS PH AND THERMOSTABILITY.
CC	EMBL: Z99106; CAB1201.1; -.	CC	-i - SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
CC	DR	DR	DR
CC	DR	PF00106; adh_short; 1.	PF00106; adh_short; 1.
CC	DR	PR00080; SDRFAMILY.	PR00106; adh_short; 1.
CC	DR	PS00061; ADH_SHORT; 1.	PR00080; SDRFAMILY.
CC	DR	KW	DR
CC	Oxidoreductase; NADP; Sporulation; Complete proteome.	Oxidoreductase; NADP (BY SIMILARITY).	PS00061; ADH_SHORT; 1.
CC	FT	FT	CC
CC	ACT_SITE 158 158 BY SIMILARITY.	ACT_SITE 158 158 NAD (BY SIMILARITY).	EMBL: D50162; BAA01476.1; -.
CC	FT	FT	CC
CC	CONFLICT 148 150 EVI -> AF (IN REF. 1).	CONFLICT 148 150 BY SIMILARITY.	EMBL: D10626; BAA01476.1; -.
CC	SQ	SQ	CC
CC	SEQUENCE 261 AA; 28090 MW; 5894C17DBBF1495 CRC64;	SEQUENCE 261 AA; 28157 MW; 6FBBC9397BCF417C CRC64;	DR
CC	Query Match 27.8%; Score 358.5; DB 1; Length 261; Matches 87; Conservative 45; Mismatches 104; Indels 21; Gaps 5;	Query Match 27.7%; Score 357.5; DB 1; Length 261; Matches 85; Conservative 51; Mismatches 100; Indels 29; Gaps 6;	DR
CC	Best Local Similarity 33.9%; Pred. No. 2.9e-22; DR	Best Local Similarity 32.1%; Pred. No. 3.5e-22; DR	InterPro: IPR002198; ADH_short.
CC	Matches 87; Conservative 45; Mismatches 104; Indels 21; Gaps 5;	Matches 85; Conservative 51; Mismatches 100; Indels 29; Gaps 6;	PR00106; adh_short; 1.
CC	Db	Db	DR
CC	5 LDGKVAITGGTGLGIAATKFKVEGAKVMT----DRHSDVGEKAAKSVGTPDQIQF 59	5 LKGKVVAITGASGLGKAMATRFGKQAKVVKVINYSNKQDPNPKVEEVKAGG----EAVV 61	PR00080; SDRFAMILY.
CC	QY	QY	DR
CC	60 FQHSSDEGWTKLDATEKAFGPVSTLVNNAGIAVAKNSVEETTAENRKLAWNLGVF 119	60 FQHSSDEGWTKLDATEKAFGPVSTLVNNAGIAVAKNSVEETTAENRKLAWNLGVF 119	PS00061; ADH_SHORT; 1.
CC	Db	Db	CC
CC	62 VQGDVTEKEDVKNYQTAIKFGTDLIMINNGLENVSPHMPKDKVIGNTLGAF 121	62 VQGDVTEKEDVKNYQTAIKFGTDLIMINNGLENVSPHMPKDKVIGNTLGAF 121	NP_BIND: 11 NAD (BY SIMILARITY).
CC	QY	QY	CC
CC	120 FGTRGLIQRMKNKGAGASINMSIEFGVFDPSLGLAYNAKSGARVIMSKAALDCALKY 179	120 FGTRGLIQRMKNKGAGASINMSIEFGVFDPSLGLAYNAKSGARVIMSKAALDCALKY 179	FT
CC	Db	Db	CC
CC	122 LGSRRAIKFVENDIKGNVNMSSVHEVIPWPLFVHAAASKGGKLWETLAKYAPK-- 179	122 LGSRRAIKFVENDIKGNVNMSSVHEVIPWPLFVHAAASKGGKLWETLAKYAPK-- 179	SEQUENCE 261 AA; 28157 MW; 6FBBC9397BCF417C CRC64;
CC	QY	QY	CC
CC	180 DRYNTVYHCGYIKTPVDDLGAEAMSQRKT----PMGHIGEPNDIAYICVYLSN 233	180 DRYNTVYHCGYIKTPVDDLGAEAMSQRKT----PMGHIGEPNDIAYICVYLSN 233	Query Match 27.7%; Score 357.5; DB 1; Length 261; Matches 85; Conservative 51; Mismatches 100; Indels 29; Gaps 6;
CC	Db	Db	CC
CC	180 GIRVNNGPGAINTP-----NAEKFADPKQKADVESWMPMGYIGEPEEIAAVAWLASK 234	180 GIRVNNGPGAINTP-----NAEKFADPKQKADVESWMPMGYIGEPEEIAAVAWLASK 234	Best Local Similarity 32.1%; Pred. No. 3.5e-22; DR
CC	QY	QY	DR
CC	234 ESKFTGSECVVDDGTT 250	234 ESKFTGSECVVDDGTT 250	MSNRLDGKVAITGGTGLGIAATKFKVEGAKVMT----DRHSDVGEKAAKSV 51
CC	Db	Db	DR
CC	235 EASYVGTITLFDAGGTT 251	235 EASYVGTITLFDAGGTT 251	1 MYDLKDRVWVITGGTGGGRAMAVFGQEEAKVVKVINYNEEALDAKKEVEEAGQAI 60
CC	DR	DR	DR
CC	RESULT 14	RESULT 15	QY
CC	DHG4_BACME STANDARD; PRT; 261 AA.	DHG2_BACME STANDARD; PRT; 261 AA.	1 MSNRLDGKVAITGGTGLGIAATKFKVEGAKVMT----DRHSDVGEKAAKSV 51
CC	P3985; 01-FEB-1995 (Rel. 31, Created)	P3983; 01-FEB-1995 (Rel. 31, Created)	172 LDCALKYDVKVWVNVHPGVYIKTPL----VDDLGAEAMSQRKT----PMGHIGEPNDIAY 225
CC	01-FEB-1995 (Rel. 31, Last sequence update)	01-FEB-1995 (Rel. 31, Last sequence update)	174 LEVAPK-GIRVNNGPGAINTP-----NAEKFADPKQKADVESWMPMGYIGEPEEIAAVAWLASK 226
CC	01-OCT-1996 (Rel. 34, Last annotation update)	01-OCT-1996 (Rel. 34, Last annotation update)	QY 226 ICVYLAESNEKSFATGSEFVVDGTT 250
CC	DE Glucose 1-dehydrogenase IV (EC 1.1.1.47) (GLCDH-IV).	DE Glucose 1-dehydrogenase II (EC 1.1.1.47) (GLCDH-II).	Db 227 VAAFLASSQASQYVTGITLEADGGTT 251
CC	GN GDHIV.	GN GDHII.	QY 227 VAFLASSQASQYVTGITLEADGGTT 251
CC	OS Bacterium; Firmicutes; Bacillales; Bacillaceae; Bacillus.	OS Bacterium; Firmicutes; Bacillales; Bacillaceae; Bacillus.	SEQUENCE FROM N.A.
CC	OC NCBI_TaxID=1404; [1]	OC NCBI_TaxID=1404; [1]	RP SEQUENCE FROM N.A.

Search completed: April 22, 2003, 17:15:45
Job time : 15 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 17:13:46 ; Search time 35 Seconds

(without alignments) (1483,539 Million cell updates/sec)

Title: US-09-910-033a-2
Perfect score: 1290
Sequence: 1 MSNRDLOCKVAILTGTLGIG.....NESKFATGSEFFVDDGGYTAQ 252

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq. length: 0
Maximum DB seq. length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_21;*

- 1: sp_archaea;*
- 2: sp_bacteria;*
- 3: sp_fungi;*
- 4: sp_human;*
- 5: sp_invertebrate;*
- 6: sp_mammal;*
- 7: sp_micr;*
- 8: sp_organelle;*
- 9: sp_phage;*
- 10: sp_plant;*
- 11: sp_rabbit;*
- 12: sp_virus;*
- 13: sp_vertebrate;*
- 14: sp_unclassified;*
- 15: sp_rvirus;*
- 16: sp_bacteriapl;*
- 17: sp_archeap;*

Pred. No. 1 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query	Match	Length	DB ID	Description
1	470	36.4	261	16	Q9ABIL	Q9abil caulobacter
2	452.5	35.1	250	2	Q937L4	Q93714 streptomyces t
3	438	34.0	254	16	Q9K4G9	Q9k4g9 streptomyce
4	427.5	33.1	244	2	Q8VL53	Q8vl53 xanthobacte
5	411	31.9	251	2	Q9RN5K	Q9rnk5 zymomonas m
6	395.5	30.7	256	2	Q93Q5	Q5287 zymomonas t
7	391	30.3	249	2	Q56841	Q93q5 brevibacter
8	388	30.1	260	17	Q8U3B3	Q56841 xanthobacte
10	386.5	30.0	247	2	Q93RM0	Q8ub3 pyrococcus
11	386.5	30.0	251	2	Q9F7E0	Q93rm0 acinetobact
12	378.5	29.3	258	2	Q9JN17	Q9f7e0 acinetobact
13	376.5	29.2	255	16	Q98ENO	Q9jn17 agrobacteri
14	374.5	29.0	248	16	Q31680	Q98eno rhizobium l
15	374.5	29.0	250	16	Q98C63	Q31680 bacillus su
16	373	28.9	249	2	Q9LBG5	Q98c63 rhizobium l

RESULT 1						
Q9ABIL	Q9ABIL	PRELIMINARY;	PRT;	261 AA.	ALIGNMENTS	
Q9ABIL;						
DT	01-JUN-2001	(TREMBLrel. 17, Created)				
DT	01-JUN-2001	(TREMBLrel. 17, Last sequence update)				
DT	01-MAR-2002	(TREMBLrel. 20, Last annotation update)				
DE	2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase.					
GN	CC0246.					
OS	Caulobacter crescentus.					
OC	Bacteria; Proteobacteria; alpha subdivision; Caulobacter group; Caulobacter.					
OX	NCBI_TaxID=15592;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=ATCC 19889 / CB15;					
RX	MEDLINE-2117368; Pubmed-11250647;					
RA	Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., ElY B., DeBoy R.T., Dodson R.J., Durkin A.S., Gruhn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Utterback T., Tran K., Wolf A., Vanathavan J.J., Emiliaeva M., White O., Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;					
RA	"Complete genome sequence of Caulobacter crescentus."					
RA	Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141 (2001).					
RA	DeBoy R.T., Dodson R.J., Durkin A.S., Gruhn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Utterback T., Tran K., Wolf A., Vanathavan J.J., Emiliaeva M., White O., Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;					
RA	"Complete genome sequence of Caulobacter crescentus."					
RA	Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141 (2001).					
RA	CC (SDR) FAMILY.					
RA	EMBL; AE00598; AAK2223.1; HSPB; P19982; IHDc.					
RA	TIGR; CC0246;					
RA	InterPro; IPR002198; ADH_short.					
RA	PRINTS; PRO0080; SDRFAMILY; PROSITE; PS0051; ADH_SHORT; UNKNOWN_1.					
KW	Oxidoreductase; Complete proteome.					
SO	SEQUENCE 261 AA; 27011 MW; CE011D872D4EB46D CRC64;					
Query	Match					
		36.4%; Score 470; DB 16; Length 261;				

Best local similarity 40.7%; Pred. No. 2.9e-27; Matches 107; Conservative 46; Mismatches 90; Indels 20; Gaps 6;	Db 240 ELVVDGGYTA 249
QY 2 SNRUDGKVKAITGGTGGGLAIATKFVEEGAKVMTDRHSVGEKAKSVGTPDQQ--- 58	RESULT 3
Db 5 TGRVAGKKAKFTGGTGGGLAIATKFVEEGAKVMTDRHSVGEKAKSVGTPDQQ--- 58	Q9KG9
QY 59 -----FQHDSSPEDGWTKLFDATKEKAFGCPVSTLVNNAGTAVNKSVEETTAERWKL 112	PRELIMINARY; PRT; 254 AA.
Db 59 GACTAFAFDVQEDOWDIDVLERATAAMGLSILVNNAGGDPESLDFGLWKKMS 118	ID 09KG9
QY 113 VNLQGVFEGTRIGQRMKWRKGGLASINNSIEGVPGDPSLGAYVAKSGAVRIMSAAL 172	AC 09KG9;
Db 119 VNVDSVFGKARHATHMRHMQPG-SIINLSSIAQINGSPATNASKRAAWL 177	DT 01-OCT-2000 (TREMBrel. 15, Last sequence update)
QY 173 DCAALKDYDVYNTVHPGKXKTPLYDPL--GAEEMMORTK-TMGHIGEPND-TAYICV 228	DT 01-JUN-2002 (TREMBrel. 21, Last annotation update)
Db 178 YCAKMKDILRSNSHPTFIDPILDFSARFKEEAKFAKLARQVPLGRIGEPTDIANAVL 237	DE Putative oxidoreductase.
QY 229 YLASNESKFATGSEFVWGGYTA 251	GN SC0169 OR SC066-06.
Db 238 YLASDESFKMTGAEIKVDOGISA 260	OS Streptomyces coelicolor.
RESULT 2	OS Bacteria; Firmicutes; Actinobacteridae; Actinomycetales; Streptomyces; Streptomyctaceae; Streptomyces.
Q937L4	OX NCBI_TaxID=1902;
ID 0937L4 PRELIMINARY; PRT; 250 AA.	RN [1]
AC 0937L4	RP SEQUENCE FROM N.A.
DT 01-DEC-2001 (TREMBrel. 19, Last sequence update)	RC STRAIN-A3(2);
DT 01-DEC-2001 (TREMBrel. 20, Last annotation update)	RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.,
DT 01-MAR-2002 (TREMBrel. 20, Last annotation update)	RL Submitted (JUN-2000) to the EMBL/GenBank/DDJB databases.
DE Cyclohexanol dehydrogenase (EC 1.1.1.1).	RN [3]
GN CPMB.	RP SEQUENCE FROM N.A.
OS Comamonas testosteroni (Pseudomonas testosteroni).	RC STRAIN-A3(2);
OC Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Comamonas.	RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.,
OX NCBI_TaxID=885;	RL Submitted (JUN-2000) to the EMBL/GenBank/DDJB databases.
RN	RN [4]
RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.
RC STRAIN-NCIMB 9872;	RC STRAIN-A3(2);
RA van Beilen J.B., Fritzsche U., Seeger M., Smits T.H.M.; Witholt B.;	RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.,
RT *Cloning of Baeyer-Villiger monooxygenases from Comamonas, xanthobacter and Rhodoboccus via PCR with highly degenerate primers.;	RL Submitted (JUN-2000) to the EMBL/GenBank/DDJB databases.
RT Submitted (NOV-2001) to the EMBL/GenBank/DDJB databases.	RN [5]
-I SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES	RP SEQUENCE FROM N.A.
CC (SDR) FAMILY.	RC STRAIN-A3(2);
CC EMBL: AJ418060; CAD10799.1; -.	RA MEDLINE-9000351; PubMed-8843436;
DR InterPro: IPR002198; ADH_short.	RA Redenbach M., Kleser H.-M., Demaute D., Eichner A., Cullum J.,
DR Pfam: PF00106; adh_short; 1.	RA Kinashi H., Hopwood D.A.;
KW Oxidoreductase.	RT "A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb streptomyces coelicolor A3(2) chromosome.";
SQ SEQUENCE 250 AA; 26626 MW; TCA42C3BAEBB858E CRC64;	RT Mol. Microbiol. 21:77-96(1996).
Query Match 35.1%; Score 452.5; DB 2; Length 250; Best Local Similarity 38.8%; Pred. No. 5.4e-26; Matches 97; Conservative 48; Mismatches 100; Indels 5; Gaps 4;	RN [4]
QY 4 RLDGKVKAITGGTGLIGIAITKEVEGAKVMTDRHSVGEKAKSVGTPDQ1QFQH- 62	RP SEQUENCE FROM N.A.
Db 3 RVNDKVVLTGGAMGMLTHCTLLAREGATVYLSDMNEELGHQVAETRQGKHAFLHL 62	RC STRAIN-A3(2);
QY 63 DSSDEDGWTKLDATEAFGPSTLVNNAGLAVNKSVEETTAERWKLAVNLQDFVFGT 122	RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.,
Db 63 DVTNENHWTGAVDTILABSDRDLALVNAGILTPVQDTSNEEDRFLFENVHSVFLGT 122	RL Submitted (JUN-2000) to the EMBL/GenBank/DDJB databases.
QY 123 RUGIQRMKNGKGLASITMSSLRGFVGPGPSLGYNASIGAVRIMSKSAAALCALDKYDV 182	RN [6]
Db 123 RAVIEPKRAHKG-C-TYNSSTYGLVGRGAAYEASCGAVRFLKACWD- LAPPNR 179	CC (SDR) FAMILY.
QY 183 VNTVHPGKIKTPVLD-LPGABEAMSQTKTPMGHIGPRNDIACVYKASNESKFATGS 241	DR HSPB; P19992; IHD.C.
Db 180 VNSVHPVVIAPMTOQILDAPOSARALLGPTLGRAAOPEMEVSOAVLFLVSDEASFVHS 239	DR InterPro: IPR002198; ADH_short.
QY 242 ERVWDGGYTA 251	DR Pfam: PF00106; adh_short; 1.
SQ SEQUENCE 254 AA; 26132 MW; A372F691F1B88672 CRC64;	DR PRINTS; PR00080; SDR_FAMILY.
Query Match 34.0%; Score 438; DB 16; Length 254; Best Local Similarity 40.7%; Pred. No. 6.6e-25; Matches 100; Indels 6; Gaps 4;	DR PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
QY 5 LDKWVAILTGGTGLIGIAITKEVEGAKVMTDRHSVGEKAKSVGTPDQ1QFQHDS 64	KW Oxidoreductase.
Db 4 LTKNVITGGARGLGAEARQAVAGAHVLTDVLLDDGENARELG- DRARFLHHDV 61	SQ SEQUENCE 254 AA; 26132 MW; A372F691F1B88672 CRC64;
QY 65 SDDGWTKLDATEAFGPSTLVNNAGLAVNKSVEETTAERWKLAVNLQDFVFGT 124	Query Match 34.0%; Score 438; DB 16; Length 254; Best Local Similarity 40.7%; Pred. No. 6.6e-25; Matches 100; Indels 6; Gaps 4;
Db 62 TSPEWWSRAADFATVTEFGALHGLVNNAGLAVNLQDFVFGT 121	Db TSPEWWSRAADFATVTEFGALHGLVNNAGLAVNLQDFVFGT 121

QY	125	GIORMKNGGASITINNNSSEFGVGPSPSLGAYNASKGAVRITMSKSALDCALKDYDVRN	184	DE
Db	122	WPALKEAG-GGSIVNISAAAGLMLGLALTAGYAGASKWGRSLTIGAVWTA--RVRN	178	OS
QY	185	TVRGKIKTPLVDDLGAEAMSQRTKTPMHIGEPRNDIAYCVYLASNEKFATGSEFV	244	Zymomonas mobilis.
Db	179	SVHPSKTYTTMAAV-GIERGEGKYNTPPMGRVEADEIGAVVFLSDAASYVTGELA	237	Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae;
QY	245	VDGGYT 250		NCBL-TaxID=542;
Db	238	VDGGWT 243		[1]
RESULT 4				SEQUENCE FROM N.A.
Q8VLS3		PRELIMINARY;	PRT;	RC STRAIN=2M4;
ID		1 :	1 :	RA Lee H.J., Kang H.S.;
AC		08VLS3;		RT "Sequence analysis of 42F4 fosmid clone of zymomonas mobilis 2M4. ";
DT	01-MAR-2002	(TREMBLrel. 20, Created)		RL "Sequence (AUG-1999) to the EMBL/GenBank/DBJ databases.;"
DT	01-MAR-2002	(TREMBLrel. 20, Last sequence update)		CC "-!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
DT	01-JUN-2002	(TREMBLrel. 21, Last annotation update)		CC DR EMBL; AF180145; AAD56922.1; -.
DE		Cyclohexanol dehydrogenase (EC 1.1.1.1) (Fragment).		DR HSSP; P19992; 1HDC.
GN				DR InterPro; IPR002198; ADH_short..
OS				DR Pfam; PF00106; adh_short; 1.
OC				DR PRINTS; PR00080; SDRFAMILY.
OC				KW Oxidoreductase.
OX		NCBI_TAXID=281;		SQ SEQUENCE 251 AA; 26621 MW; 62DD151CAF7CF6B CRC64;
RN		[1]		Query Match 31.9%; Score 41; DB 2; Length 251;
RC		SEQUENCE FROM N.A.		Best Local Similarity 40.6%; Pred. No. 6.6e-23;
STRAIN=ZL5;				Matches 101; Conservative 33; Mismatches 95; Indels 20; Gaps 0;
RA		van Beilen J.B., Fritsche U., Seeger M., Smits T.H.M., Witholt B.;		QY 14 GGTIGIGLAIATEKVEEGAKVMTDRHSDGKEAKAAS-VGTPDQIOFFQDSSDEGWTKL 73
RA		"Cloning of Baeyer-Villiger monooxygenases from Comamonas, xanthobacter and Rhodococcus via PCR with highly degenerate primers.;"		Db 5 GCARGIGRAIAAAFQHEGAKVIVTDIDEVGKTKTAEIGG---QFKLDRREKDQNL 60
RA		Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.		QY 74 FDATEKARGPVSTLVNNAGI-----AVNSVSRVTTAEWRKLAVLNLDGVFGRTRGIO 127
RA		EMBL: AJ418061; CAD0802.1; -.		Db 61 AETVPP---WVDVVWNNAAGITGFENGAVAHDPERHATLEDWRAVHRVNLDGCFGLGRYIA.116
DR		InterPro: IPR002198; ADH_short.		QY 128 RMKNKGGLGASINNSISLGFGVGPSPSLGAYNASKGAVRIMSKSALDCALKDYDVRN 187
DR		PFAM: PF00106; adh_short; 1.		Db 117 AMKNGKTG-SIINISRSGLVQGIPLLAAVASSKRAIRHNSKVALYCAQGKIRCNAIN 175
DR		PRINTS; PR00080; SDRFAMILY.		QY 188 PGITKTPPLVDDLGAEAMSQRTKTPMHIGEPRNDIAYCVYLASNEKFATGSE 242
KW		Oxidoreductase.		Db 176 PAALITSIWPEMLGDDREKRQMLVALDTPLRKGLEEEVAVAVMLASDEATYMGAE 235
FT		NON_TER 244 AA; 2550 MW; 01FC9B7101CC1B8P CRC64;		QY 243 FVFDGGYT 251
FT		SEQUENCE 244 AA; 2550 MW; 01FC9B7101CC1B8P CRC64;		Db 236 FNIDGGLLA 244
Matches	103;	Best Local Similarity 33.1%; Score 427.5; DB 2; Length 244;		
Matches	103;	Conservative 36; Mismatches 96; Indels 15; Gaps 6;		
QY	4	RLDGKVATIGGGTUGIGLATAKTFVEEGAKVMTDRHSDGKEAKAAS-VGTPDQIOFFQDSSDEGWTKL 62		RESULT 6
Db	3	RVQDKVVALVGGAMGKGGRTHETLAAEGAVVFGDRDAAGKAVAKGKGAEFLS 62		Q52587 PRELIMINARY; PRT; 254 AA.
QY	63	DSSDEGWTIILEDTEKAFFPVSTLVNNAGIATVNSVVEETTAERWLKLLAVNLDGVFFGT 122		ID Q52587
Db	63	DVTKESSDWAIAVDTVAKSKKLNVLNVNAGIATVLSVLPKAHETTENDSTENVNVRGWLGI 122		AC 052587;
OY	123	RLGIORMKNGGASITINNSISLGFGVGPSPSLGAYNASKGAVRIMSKSALDCALKDYDVR 182		DT 01-NOV-1996 (TREMBLrel. 01, Created).
Db	123	RSFVPLM--KGNNGLNITISIISIYIGVAGPAGAYIASKGAVRLITKSCAVD--LFGFIR 178		DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
OY	183	VNTVHGYIYKPLVDDL---PGAEAMSQRTKTPMHIGEPRNDIAYCVYLASNEKFATGSE 236		DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
Db	179	VNSVHGVQVITPMKDLLHGDPAARKAIGMATEFLDRPC---QPVESKAVLFLASDES 234		DE Beta-hydroxysteroid dehydrogenase.
OY	237	FATGSEFWD 246		OS Comamonas testosterone (Pseudomonas testosterone).
Db	235	FVHGAEMVVD 244		OC Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Comamonas.
RESULT 5				CC DR STRAIN=ATCC 11996;
Q9RNK5				CC DR STRAIN=ATCC 11996;
ID		PRELIMINARY;	PRT;	RA Cabrera J.E., Gent-Raimondi S.;
AC		1 :	1 :	RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DT	01-MAY-2000	(TREMBLrel. 13, Created)		CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
DT	01-May-2000	(TREMBLrel. 13, Last sequence update)		CC DR EMBL; U01265; AAA25742.1; -.
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)		DR HSSP; P19992; 1HDC.
DR		InterPro; IPR002198; ADH_short.		DR InterPro; IPR002198; ADH_short.
DR		Pfam; PF00106; adh_short; 1.		DR Pfam; PF00106; adh_short; 1.
DR		PRINTS; PR00080; SDRFAMILY.		DR InterPro; IPR002198; ADH_short.
DR		ROSIKE; PS00061; ADH_SHORT; UNKNOWN_1.		DR ROSEIKE; PS00061; ADH_SHORT; UNKNOWN_1.
KW		Oxidoreductase.		DR SEQUENCE 254 AA; 26952 MW; FB6EC0B151975DB CRC64;

Query Match	31.9%	Score 411; DB 2; Length 254;
Best Local Similarity	36.8%	Pred. No. 6.7e-23;
Matches	92;	Conservative 48; Mismatches 102; Indels 8; Gaps 4;
Qy	1	MSNRDCKVAVITGGTIGGLAIATKEVEEGAKVMTDRHSVGEKAASKVTPDQIQQFF 60
Db	1	MTRNQCKVALVTTGGASGVGLLEVKKLGEGRKAQVAFSDINERAGQQLAAEIG--ERSMFV 58
Qy	61	QHDSSDEGWTKLFDATKEAFGPVSTLVNNAGIAVNNKSVETTAEWRKLAVNLGDVFF 120
Db	59	RHDVSSBADMVTLVMAAVORRIGTTLVNLVNNAGILLQGDMETGRLEPSRLKINNTSVFI 118
Qy	121	GTRLGQRMKNGLGLASINNMSIEGVGDPDSLGAQVAKVMSKAAALDCALKDYD 180
Db	119	GCQQGTAAMKE--TGGSIINMSVSSWLPQYQYASAKAVSLJTRAAALSCRKOGYA 176
Qy	181	VRVNTVHPGYIKTPVLD-DLP---GAEAMSQRTKIPGMHIGEPNDIAYIVCVYLASNEK 236
Db	177	IRVNTHPDGYTPMNOASLPKGVSKEMVLHDPKLNRAGRAYMPERIAQLVFLASDESS 236
Qy	237	FATGSEVVD 246
Db	237	VMSGSLHAD 246
RESULT 7		
Q93QG5		PRELIMINARY; PRT; 256 AA.
AC	Q93QG5	
DT	01-DEC-2001	(TREMBLrel. 19, Created)
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)
DT	01-MAR-2002	(TREMBLrel. 20, Last annotation update)
DE	Cyclohexanol dehydrogenase.	
GN	CNA.	
OS	Brevibacterium sp. HCU.	
OC	Actinomycetales; Micrococcineae; Brevibacteriaceae; Brevibacterium.	
OX	NCBI_TAXID=133406;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=HCU;	
RA	BROSTOWICZ, P.C., BLASKO, M.S.; Rouviere, P.E.;	
RT	"Identification of Two Gene Clusters Involved in Cyclohexanone in Brevibacterium sp. HCU.,"	
RL	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.	
CC	-1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.	
CC	(SDR) FAMILY.	
DR	EMBL: X79853; CAA56245.1; -.	
DR	HSSP: P19992; 1HDC.	
DR	InterPro: IPR00198; ADH_short.	
DR	Pfam: PF00106; adh_short; 1.	
DR	PRINTS: PRO0080; SDR_FAMILY.	
DR	PROSITE: PS00061; ADH_SHORT; UNKNOWN1.	
KW	Oxidoreductase.	
SEQUENCE	249 AA; 24940 MW; B5E0B82C1D8D9782 CRC64;	
Query Match	30.3%	Score 391; DB 2; Length 249;
Best Local Similarity	38.9%	Pred. No. 2e-21;
Matches	98;	Conservative 39; Mismatches 105; Indels 10; Gaps 6;
Qy	5	LDGKVAITGGTIGGLAIATKVEEGAKVMTDRHSVGEKAASKVTPDQIQQFQHDS 64
Db	2	LDAAVIAITGGAGIGLAVAHAIAGARVYALIDRGACAGAAAEFGA--AAMGVGADY 59
Qy	65	SDEDGWTKLFDATKEAFGPVSTLVNNAGIAVNNKSVETTAEWRKLAVNLGDVFFGTRL 124
Db	60	TDEAAITAAMAGAQARALGPETGLVNNAGIAGFGSHATEVETWSRIMAVNTGTRFLASKA 119
Qy	125	GIORUMKNGIGASINTNSSTEGFVDPDSLGAQVAKVMSKAAALDCALKDYDVRN 184
Db	120	ALFGMLERGRGA-TNFGSTPAGLVGIPTMAMCANKGAVNLTROMADSGR--GIRVN 176
Qy	185	TVHRSYIK-TPLVDDLGAE---EAMSQRTKTPMIGHIGEPNDIAYIVCVYLASNEKF 239
Db	177	WVCPGTVAGTDMGRQLGTDCDPELEARRLAKYPMGFGTPEIAAEVFLSTKAAFT 236
Qy	240	GSEFFVDDGTA 251
Db	237	GSVLAVIDGGMTA 248
RESULT 9		
Q8UJB3		PRELIMINARY; PRT; 260 AA.
ID	Q8UJB3	
AC		
DT	01-JUN-2002	(TREMBLrel. 21, Created)
DT	01-JUN-2002	(TREMBLrel. 21, Last sequence update)
DT	01-JUN-2002	(TREMBLrel. 21, Last annotation update)
DE	3-oxoacyl-1-facyl-carrier protein] reductase.	
GN	PF0057	
OS	Pyrococcus furiosus.	

OC	Archaea: Euryarchaeota: Thermococcales: Thermococcaceae;
OX	Pyrococcus.
RN	NCBI_TAXID-2261;
RP	[11]
SEQUENCE FROM N.A.	
STRAIN=VC1 / DSM 3638 / ATCC 43587 / JCM 8422;	
RA	Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT	"The complete sequence of the Pyrococcus furiosus genome."
RL	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AE010178; AAL80681.1; -.
KW	Complete proteome.
SQ	SEQUENCE 260 AA; 28367 MW; 0DD71F0B3C665286 CRC64;
Query Match	30.1%; Score 388; DB 17; Length 260;
Best Local Similarity	36.4%; Pred. No. 3.5e-21;
Matches	95; Conservative 43; Mismatches 99; Indels 24; Gaps 6;
OY	5 LDGKVAITGGTGGIGLALATKVEEGAKVMTDRHSDVG-EKAASKVGTPOQIOFFQHD 63
Db	6 LKNNKVATVGGGOGIGAAIAOLFRENGAKVVAEIDEAEGLEEARMLERGLDUTFIKD-65
OY	64 SSDEDGWTKLFDATKEAAGPVSTLVNNAGIANNAGVNSVEETTAEWRLKLAVNLGUVFGTR 123
Db	65 VADEEESTKNNMKVKTVELYGGVLDLVNNAAIMSVKSIFERPLEEWVIRVNLGTVPICSR 125
OY	124 LGIORMKNGLGASITINNSIEGFGDPLGAYNASKGAVRIMSKAALDCALKDVKYRV 183
Db	126 YAAEEMIKRG-GGVINIASTRALMSEPTEPISASKGIGLALTHSLAI--SLAKYRIRV 182
OY	184 NTVHHPGTYKT-----PLVDDPGAEAEAMSQRTKPPMGHGEPPNDIAYICVYLAS 232
Db	183 VAVSPGWIETSRWKSKLRLSEPKLRPI-----DHEQHPAGRVGDPMPDIAHICAFLAD 234
OY	233 NE-SKFTGSEFVVDGGYTAQ 252
Db	235 NEKAGFTGVNFWDGGMVK 255
RESULT 10	
093RMO	PRELIMINARY; PRT; 247 AA.
ID	093RMO:
AC	093RMO;
DT	01-DEC-2001 (TREMBrel. 19, Created)
DT	01-DEC-2001 (TREMBrel. 19, Last sequence update)
DT	01-JUN-2002 (TREMBrel. 21, Last annotation update)
DE	Cyclohexanol dehydrogenase.
GN	CHNA.
OS	Acinetobacter sp. SE19.
OC	Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
OC	Acinetobacter.
OX	NCBI_TaxID-135835;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=SE19;
RX	MEDLINE-2038154; PubMed-10940013;
RA	Cheng Q., Thomas S.M., Kostichka K., Valentine J.R., Nagarajan V. "Genetic analysis of a gene cluster for cyclohexanol oxidation in acinetobacter sp. strain SE19 by in vitro transposition.";
RT	J. Bacteriol. 182:4744-4751 (2000).
RL	-
CC	-I- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SR) FAMILY
DR	EMBL; AF282240; AAG10026.1; -.
DR	HSSP; P19992; 1HDC.
DR	InterPro; IPR002198; ADH_short.
DR	ProDom; PF00106; adh_short; 1.
DR	PRINTS; PR00080; SDRFAMILY.
DR	PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
KW	Oxidoreductase.
SQ	SEQUENCE 251 AA; 26159 MW; B3BA48055997D5D CRC64;
Query Match	30.0%; Score 386.5; DB 2; Length 251;
Best Local Similarity	33.7%; Pred. No. 4.3e-21;
Matches	86; Conservative 60; Mismatches 98; Indels 11; Gaps 6;
OY	1 MSNRDCKVAITGGTGGIGLALATKVEEGAKVMTDRHSDVGKAA-KSVGTPOQIF 59
Db	5 MSNKNKVALTGGSGIGKSTALLAQAQVSDINLEAAQVDRDVALGCKAA 64
OY	60 FOHDSSDEDGWTKLFDATKEAAGPVSTLVNNAGI-ANVKVEETTAEWRLKLAVNLG 117
Db	65 NKANTAAEPEDMKAKEVAPVSTGCAHLAFLNAGNAGTGEVN-STEELSIEGMRVTDVNLNA 123
OY	118 VFFGTRGLIQRMKNGLGASITINNSIEGFGDPLGAYNASKGAVRIMSKAALDCALK 177
Db	124 VFSMHHYEVPAILAG-GGAVINTASTAGLIGQNIISGVAAKHGTGLKAMALEYA-- 180
OY	178 DYDVRNTVHCGYIKTLPUDLPGAEAMSQRTKPPMGHGEPPNDIAYICVYLASNEKF 237
Db	181 DKGTRINSHVPGYIKTPLIAEREAEMVKLH---PIGRGQPEEVAQVWAFLSDDASF 236
OY	238 ATGSEFVVDGGYTAQ 252

RP	SEQUENCE FROM N.A.	RESULT 15
RC		09BC63
RX		09BC63
RA		PRELIMINARY; PRT; 250 AA.
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchart S.,	ID	09BC63; AC
Borriell R., Bourlier L., Brans A., Brun M., Brignell S.C., Bron S.,	DT	01-OCT-2001 (TREMBrel: 18, Created)
Broillet S., Bruschi C.V., Caldwell V., Carter N.M.,	DT	01-OCT-2001 (TREMBrel: 18, Last sequence update)
Choi S.K., Codani J.J., Conneron I.F., Cummings N.J., Daniel R.A.,	DE	Glucose dehydrogenase.
Denizot F., Devine K.M., Dusterhoff A., Ehrlich S.D., Emmerson P.T.,	GN	MUR5280.
Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,	OS	Rhizobium loti (Mesorhizobium loti)
Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,	OC	Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Ghim S.Y., Glaser P., Gofreau A., Golightly E.J., Grandi G.,	OC	Phyllobacteriaceae; Mesorhizobium.
Guliseppi G., Guy B.J., Haga K., Hailech J., Harwood C.R., Henaut A.,	OC	NCBI_TaxID:381;
Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,	RN	[1]
Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,	RN	SEQUENCE FROM N.A.
Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,	RN	SEARCHED
Kurita K., Lapicis A., Lardinois S., Lauber J., Lazarevic V.,	RX	STRAIN-MAFF03099;
Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,	RX	MEDLINE-2102930; Pubmed-12114968;
Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,	RA	Kanebo T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oueda B., Park S.H.,	RA	Watanabe A., Idezawa K., Isikawa Y., Kohara M., Kawashima K., Kimura T.,
Parro V., Pohl T.M., Portelette D., Porwollik S., Prescott A.M.,	RA	Kishida T., Kiyokawa C., Kohara M., Matsunoto M., Matsuno A.,
Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,	RA	Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,	RA	"Complete genome structure of the nitrogen-fixing symbiotic bacterium
Sato T., Scanlan E., Schlech S., Schnoerter R., Scoffone F.,	RT	Mesorhizobium loti."
Seikiguchi J., Sekowska A., Serror S.J., Serror P., Shin B.S., Soldo B.,	RL	DNA Res. 7:331-338.
Sorokin A., Tacconi E., Tagagi T., Takahashi H., Takeda K.,	DR	EMBL; AP003006; BAB51758.1; -.
Takeuchi M., Tamakoshi A., Tanaka T., Terpsira P., Tognoni A.,	DR	InterPro; IPR002198; ADH_short.
Tosato V., Uchiyama S., Vandenberg M., Vanner F., Vassarotti A.,	DR	PFAM; PF00106; adh_short; 1.
Viani A., Wambutt R., Wedler E., Wedler H., Weizenecker T.,	DR	PRINTS; PR00080; SDRFAMILY.
Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,	KW	Complete proteome.
Yoshida K., Yoshikawa H., Yoshikawa H., Danchin A.,	SO	SEQUENCE 250 AA.; 26407 MW; 1736D8C3F6711274 CRC64;
RT		Query Match 29.0%; Score 374.5; DB 16; Length 250;
RL		Best Local Similarity 37.1%; Pred No. 3.4e-20;
RN	[2]	Matches 93; Conservative 47; N mismatches 98; Indels 13; Gaps 5;
RP	SEQUENCE FROM N.A.	Query 4 RLDGKVAILITGEGMGLIATKVFVEGAKVMTDRISDVGEAKSGUTPQDQIQRHD 63
RC		Db 3 KLEGKIAWITGGSSGIGLATAKRFVERGAVHVVITGRRELKELAAFI-MRNVTIVGD 60
RX		Query 64 SSDEDGKTKLDFATEKRGPVSTLVNNAGIANKSVEETTAERKLAVALNLDGVFFSTR 123
CC	-1 SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES	Db 1 P4227; IBOB.
CC	(SDR) FAMILY	Db 2 InterPro; IPR002198; ADH_short.
DR	EMBL; Z99111; CAB13250.1; -	Db 3 Pfam; PF00106; adh_short; 1.
DR	HSSP; P4227; IBOB.	Db 4 P00080; SDRFAMILY.
DR	InterPro; IPR002198; ADH_short.	Db 5 Complete proteome.
DR	Pfam; PF00106; adh_short; 1.	Db 61 VSLLEDIPLRDYAVVKEKHHIYLFANGAGTIAPLAAEATFQDTPDYNVKGLEFV 120
KW	Oxidoreductase; Complete proteome.	Db 124 LGIORMKNGLGASININNSISGFVGDSLGLAYNASKAVRIMSKSALDCAALKDYRV 183
SEQUENCE	248 AA; 26245 MW; EACA490C1239524D CRC64;	Db 121 KALPLKD--GGSIILINSSVSNVLGRLGFGSTYIAASKAVRNFSRAWLE-LKDRKIRV 175
Query Match 29.0%; Score 374.5; DB 16; Length 248;	Query 184 NTVHPGKTIKPLVDDLG---AEEAM-SQRTKPMGHGEPNDIAYCVYLASHESKF 237	Db 176 NMSPGAIETPALETRGTLTPEQAEQAWAQSOQIPMRRGKPEEIAAVTFLASDDSY 235
Best Local Similarity 37.5%; Pred. No. 3.3e-20;	Db 177 NWSPGCLTIPADELFGDALEEVLEENSRNTWFGKVKTPPEEANAVNSFLASDESSY 236	Db 238 ATGSEFVDDG 248
Matches 93; Conservative 40; Mismatches 106; Indels 9; Gaps 5;	Db 236 VTGVDAVDGG 246	Search completed: April 22, 2003, 17:16:27
QY	4 RLDGKVAILITGEGMGLIATKVFVEGAKVMTDRISDVGEAKSGUTPQDQIQRHD 63	Job time : 38 'secs
Db	3 KFEGKIALVIGGSGIGLATAKRFVERGAVHVVITGRRELKELAAFI-MRNVTIVGD 60	
QY	64 SSDEDGKTKLDFATEKRGPVSTLVNNAGIANKSVEETTAERKLAVALNLDGVFFSTR 123	
Db	121 KALPLKD--GGSIILINSSVSNVLGRLGFGSTYIAASKAVRNFSRAWLE-LKDRKIRV 175	
Db	124 LGIORMKNGLGASININNSISGFVGDSLGLAYNASKAVRIMSKSALDCAALKDYRV 183	
QY	184 NTVHPGKTIKPLVDDLG---AEEAM-SQRTKPMGHGEPNDIAYCVYLASHESKF 237	
Db	177 NWSPGCLTIPADELFGDALEEVLEENSRNTWFGKVKTPPEEANAVNSFLASDESSY 236	
QY	241 SEFWVPGG 248	
Db	237 VELFLVDOG 244	